



# Sequence Listing

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Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Hillan, Kenneth J  
Kljavin, Ivar J.  
Kuo, Sophia S.  
Napier, Mary A.  
Pan, James;  
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Roy, Margaret Ann  
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Wood, William I.
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Ala Ala Thr Glu	Ala Val Ala Ile Leu	Thr Ala Thr Tyr Pro	Val	275	285
Gly His Met Pro	Tyr Gly Trp Leu Thr	Glu Ile Arg Ala Val	Tyr	290	300
Pro Ala Phe Asp	Lys Asn Asn Pro Ser	Asn Lys Leu Val Ser	Thr	305	315
Ser Asn Thr Val	Thr Ala Ala His Ile	Lys Lys Phe Thr Phe	Val	320	330
Cys Met Ala Leu	Ser Leu Thr Leu Cys	Phe Val Met Phe Trp	Thr	335	345
Pro Asn Val Ser	Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val	Asp	350	360
Phe Ala Phe Ala	Glu Leu Cys Val Val	Pro Leu Arg Ile Phe	Ser	365	375
Phe Phe Pro Val	Pro Val Thr Val Arg	Ala His Leu Thr Gly	Trp	380	390
Leu Met Thr Leu	Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser	Val	395	405
Leu Arg Ile Ile	Val Leu Ile Ala Ser	Leu Val Val Leu Pro	Tyr	410	420
Leu Gly Val His	Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu	Ala	425	435
Gly Phe Val Gly	Glu Ser Thr Met Val	Ala Ile Ala Ala Cys	Tyr	440	450
Val Tyr Arg Lys	Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala	Thr	455	465
Glu Gly Glu Asp	Ser Ala Met Thr Asp	Met Pro Pro Thr Glu	Glu	470	480
Val Thr Asp Ile	Val Glu Met Arg Glu	Glu Asn Glu		485	490

<210> 8  
<211> 335  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 66, 96, 387  
<223> unknown base

<400> 8  
octacagaa gtgcacccgga gctggggggag atncaacatt aagaagatgc 50  
tgajortctg gtgccontttg gctctaatto tggccacaca gagaancagt 100  
cggtctcttg tcaacctctt tgtttcccgg gaccttgggtg gcagttctgc 150  
agccacagag gcagtgggga ttttgacaga cacataacct gtgggtcaca 200  
tggcatcgg ctggttgacg gaaatccgtg ctgtgtatcc tgccttcgac 250  
aagaataacc ccagcaacaa actgggtgagc acgagcaaca cagtcacggc 300  
agtcacacac aagaagtcca ccttcgtctg catgggtctg tcaactcagc 350  
tcgtttcgt gatgttttg acacccaaag tgtctgngaa aatcttgata 400  
gacatctctg gactggactt tgcctttgca gaactctgt tcttcccttc 450  
acgcatcttc cctttcttcc cagttccagt cacagtgagg gcgcatctca 500  
ccagtggct gatgacaact aagaaaacct tcttc 535

<210> 9  
<211> 434  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 328, 273,  
243, 296, 305, 336, 353, 361  
<223> unknown base

<400> 9  
tgaagggaac ccgggctggg tatctgggt tngacaagat aaacccccag 50  
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100  
agttcaacct ngtttgnatg gntctgtcaa ctcaagctnt gtttcgtgat 150  
gtttttggaa cccaaagtgt ttgagaaaat ttgatagac atnatcggag 200  
tggantctg ctttgcagaa ntttgnntg ttcttttgg gattttctcc 250  
tttttccag ttccagtcac agngagggcg catctcaccg gnggntgat 300



gicantgaag aaaaacatttg tccctgcccc cagctntttg gtgaggatca 350  
tctgtccnat nccagacatt gtggctctac cctacctggg ggtgcacggt 400  
ggagacattg gctggggttc cctcctggcg ggca 434

<210> 10  
<211> 154  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 49, 63, 83, 90, 93, 119  
<223> unknown base

<400> 10  
tattccagat tccggccacg gggagggggc atntcacagg gtggctgang 50  
aaactgaaga aaacatttngt ccttgcaccc agntttgtgn tgaggatnat 100  
tggctccatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150  
area 154

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
cagatccggg tcttggtgac cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgacac tcaagctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcattctctt cctctccc 18

<211> 14  
<211> 13  
<211> DNA  
<211> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccctccgcc cggagttc 18

<211> 15  
<211> 24  
<211> DNA  
<211> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
ggcaaatcc actccgatga tgtc 24

<211> 16  
<211> 24  
<211> DNA  
<211> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
gcatgggtg gtcacaggtc tccg 24

<211> 17  
<211> 45  
<211> DNA  
<211> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcggggagca ggccctgaac cggggcattg ctgctgtcaa ggagg 45

<211> 18  
<211> 1901  
<211> DNA  
<211> Homo sapiens

<400> 18  
gccccggccc cggcgccggg cgcgccgagc cgggagccac cggcatgggg 50  
gcatgcatgg gaggctgctc cctgctcagc tgcgcgtcct gactctgcgg 100  
ctctgccccc tgcctcctgt gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200  
 tccatcatta tgcctgagccc gggcgtggag agtcagctct accagctgcc 250  
 ctgggtgtgt gaggaggggg ccgggatccc caccgtctg cagggccaca 300  
 ccgactgtgt ctccctgctt gggtaccggg ctgtctaccg catgtcttc 350  
 gccacggggg ccttcttctt ctctcttttc acctgctca tgcctgggt 400  
 gagcagcagc cgggaccccc gggctggcat ccagaatggg tcttggtct 450  
 ctaagttcat gatcctgggt gggtccaccg tgggtgcctt ctacatccct 500  
 gacggctcct ccaccaacat ctgggtctac ccggggtcg tgggtcctt 550  
 cctcttcctc ctcatccagc tgggtgtgt ctctgactt gccactcct 600  
 ggaaccagcg gtggctgggg aaggccgagg agtgcgattc ccgtgcctgg 650  
 taccgaggcc tcttcttctt cactctcttc ttctacttgc tctcgatcgc 700  
 ggccgtggcg ctgatgtca tgtactacac cgagccagc ggtgcacag 750  
 agggcaaggt ctctatcagc cccaacctca cctctgtgt ctgggtgtc 800  
 atcgtgtctg cctgcacca ggtccaggac gccagacca actcgggtct 850  
 gctgcaggcc ccgtccatca cctctacac catgtctgt acctggtcag 900  
 ccttatccag tatccctgaa cagaaatgca accccatct gccaacccag 950  
 ctgggcaacg agacagttgt ggcaggcccc gagggctat gagccagt 1000  
 gtgggatgcc ccgagcattg tgggcctcat catctcttc ctgtgcaccc 1050  
 ccttcacag cctgcgctcc ccagaccacc ggcagggtgaa cagcctgatg 1100  
 cagacccagg agtgccaccc tatgtagac gccacacagc agcagcagca 1150  
 gcagggtggc gctgtgagg gcggggcctt tgaacaagag caggacggcg 1200  
 tcaactacag ctactccttc ttccactct gctgggtgt ggcctcact 1250  
 cactcatga tgaagctcac caactggtaa aagcccggtg agaccggga 1300  
 gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
 cagggctgt cctctactg tggacctgg tagcccaact cctcctggcg 1400  
 aaccccgact ccagctgagg cagcctcaca gctgcacac tgggtgcctc 1450  
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 caccaatcag ccaggctgag ccccaacccc tggccagct ccaggacctg 1550  
 cccctgagcc gggccttcta gtgtagtgc ctccagggtc ccaggagcat 1600

cagggtccttg cagagcccca tccccccgac acacccacac ggtggagctg 1650  
 cctcttcctt cccctctctc ctgttgccca tactcagcat ctgggatgaa 1700  
 agggctccct tgtctcagg ctccacggga ggggggctgc tggagagaga 1750  
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctgggtgttc 1800  
 tggtaagtc ccccagggga cctgcccccc ctctgggact tctgtcctta 1850  
 ctgagtctct aagacttttt ctaataaaca agccagtggg tgtaaaaaaa 1900  
 a 1901

<210> 19  
 <211> 457  
 <212> PRT  
 <213> Homo sapiens

<210> 19  
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser  
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 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro  
 20 25 30  
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe  
 35 40 45  
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly  
 50 55 60  
 Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly  
 65 70 75  
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser  
 80 85 90  
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala  
 95 100 105  
 Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser  
 110 115 120  
 Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe  
 125 130 135  
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr  
 140 145 150  
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val  
 155 160 165  
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile  
 170 175 180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu	135	136	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr	196	205	215
Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe	216	227	228
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala	241	251	255
Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser	455		

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
gagggatcat attcacgttc ttcc 24

<210> 11  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
tcatctagct ggtgctgctc 20

<210> 22  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 21  
cttcttccac ttctgctgg 20

<210> 23  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 19  
ctctgggcaca aatgcaac 18

<210> 14  
<211> 14  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
caggaatgta gaaggcacc acgg 24

<210> 25  
<211> 24

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<216> 25

tggaagagat attcaacacac acgg 24

<216> 26

<217> 50

<218> DNA

<219> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<222> 26

gttccatcat tatgtgagc cggggcgtgg agagtcagct ctacaagctg 50

<223> 27

<224> 1351

<225> DNA

<226> Homo sapiens

<227> 27

gagcagggcc ggggaactgaa ggtgtgggtg ccgagccctc tggcagaggg 50

ttaacctggg tcaaatgcac ggattctcac ctgtacagt tacgtctctc 100

cgggcacgt ccgagaggac ttgaagtccg gagcgctcaa gtttgcctgt 150

aggtcagag agggccatgg aggtgcggcc accggcaccc cggagctttc 200

ctctagagc attgtgccta tttcccgag cctctgtgc cgaagctgtg 250

actgcagatt cgggaagctc tgaggagcgt cagaagcggc tccctacgt 300

cccagagccc tattaccgg aatctggat ggaccgccc cgggagctgt 350

tggcraaga tgaacagcag agaatttcaa aggaacttgc taatatctgt 400

aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450

agcttttatt catgctaaac aacaatacat cgagcagagc caggcagaaa 500

tttatataa ccggtttgat gctgtgcaat ctgcacatcg tgotgcacac 550

caggcttcca ttogttatgg ctggcgctgg ggttgagaaa ctgcagtgtt 600

tgtgactata ttcaacacag tgaacactag ctctgaatgta taacgaaata 650

aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700

tttaggataa acgtaggcct gctgtggcctg gtggctgggt gcataattgg 750

agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800

acgctgggtga gactgttcag gaaagaaaaac agaaggatcg aaaggpactc 850  
 catgagctaa aactggaaga gtggaaagga agactacaag ttactgagca 900  
 cctccctgag aaaattgaaa gtagtcttacg ggaagatgaa cctgagaatg 950  
 atgctaagaa aattgaagca ctgctaaaac ttcttagaaa cctttcagta 1000  
 atagataaac aagacaagga ctgaaagtgc totgaacttg aaactcactg 1050  
 gagagctgaa gggagctgac atgtccgatg aatgccaaca gacagggcac 1100  
 cctctgggtca gctgctgac aaatttaagt gctggtaccc gtgggtggcag 1150  
 tggcttgccc ttgtctttt cttttctttt taactaagaa tgggggtgtt 1200  
 gtaactctac ttactctac cttaaattta aatactact tatgtttgta 1250  
 ttaattctac aatatatgca tacatggata tatoracca cctagatttt 1300  
 aagcagtaaa taaaacattt cgcaaaagat taaagtgaa ttttacagtt 1350  
 t 1351

<210> 23  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
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 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
 20 25 30  
 Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val  
 35 40 45  
 Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu  
 50 55 60  
 Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala  
 65 70 75  
 Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val  
 80 85 90  
 Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile  
 95 100 105  
 Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val  
 110 115 120  
 Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly  
 125 130 135



Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn
				140					145					150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu
				155					160					165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg
				170					175					180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly
				185					190					195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln
				200					205					210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg
				215					220					225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu
				230					235					240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg
				245					250					255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu
				260					265					270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp
				275					280					285

<210> 29  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 gggaagtcac ttgaggagcg tcagaagcgg ctccactacg tccagagac 50  
 ctatcaccg gaatctggat gggacgcctc cgggagctgt ttggcaaaga 100  
 tgaacagcag agaatttcac aggaacttgc taatatctgt aagaaggcag 150  
 ctatagcagg catcattggc tgggtgtatg ggggaataac agcttttatt 200  
 catgctcaac aacaatacat tgagcagagc caggcagaaa ttatcataa 250  
 cccatttgat gctgtgcaat ctgcacatcg tctgtgcaca cgaggcttca 300  
 ttgtttatg gctggcgccg aacc 324

<210> 31  
 <211> 317  
 <212> DNA  
 <213> Homo sapiens

<220>

<201> unsure  
<202> 262, 330, 371  
<203> unknown base

<400> 30  
tcaagtttgt ccgtaggctg agagaaggcc atggaggtgc cgcacccggc 50  
acccgcgtagc tttttttctgt agagcattgt gctattttcc ccgagtttt 100  
gtcgcacaag ctgtgactgc cgattcggaa gtcccttgagg agcgtcagaa 150  
cagccttccc taactccacg agccctatta cccggaattt ggatgggacc 200  
gcctcccgga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
cttgcgtata ttgtgaagac ggcagctaca gcaggcatca ttggctgggt 300  
ctatggggga ataccagctt ctattcatgn taaacaacaa tacattgagc 350  
agagccaggc agaaatttat nataacc 377

<210> 31  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 31  
tgcctacgtt acgctctccc 20

<210> 30  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 31  
cttcagtagc gtcagaagcg 20

<210> 30  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 30  
ataacgcatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA

<013> Artificial Sequence

<020>

<025> Synthetic oligonucleotide probe

<400> 34

ataaatatct gtaagacggc agctacagca ggcatcattg 40

<010> 35

<011> 1-19

<012> DNA

<015> Homo sapiens

<400> 35

gagcgcgcgc ccgcgcgcgc ccgcgcactg cagccccagg ccccggcgcc 50  
ccacccacgt ccgcgttgcg gccccgcctg ggccaggccc caaaggccaag 100  
gacaaagcag ctgtcagggg acctccgcgc gagtccaatt tacgtgcagg 150  
tgcgggcaac cacaggttcc aagatgggtt gggggggctt ccggtgttcc 200  
aagcaactgc ctgcgcgcct caacctgctt cacacctggg ctagtctgct 250  
gtcaattgga attgctgcgt ggggcattgg cttcgggctg attccagctc 300  
tcgcagtggt ccggttggtc attgcagtgg gcattctctt gttccctgatt 350  
gtttttagtg gtctgattgg agctgtaaaa catcatcagg cgttcctatt 400  
tttttatatg attattctgt tactctgatt tattgttcag tttctctgat 450  
cttcgccttg tttagccctg aaccaggagg aacagggtca gttctcggag 500  
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aaaactgctgt gggctccgaa gtgttaaccc aaatgacacc tgtctggcta 600  
gtctgtgtta aagtgaaccs cctgtctctg catgtgctcc aatcatagga 650  
gaatatgctg gagagggttt gagatttgtt ggtgggcatt gctgtctctt 700  
cagttctaca gagatcctgg gtgtttggct gaactacaga tacaggaacc 750  
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caagatttcc ttcgttatta tgatcttgtt cactttctgt aattttctgt 850  
taagctccat ttgcacgttc aaggaaggaa acactatctg gaaaagtacc 900  
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tctttcttcc gttgctgaaa aatatttgaa acctgtggct tcctgaagctc 1000  
cgtggcacct ggaatttact gtattcatcg tcgggcactg tcactgttg 1050  
cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcaactggtat aattatatgt 1150  
 agcactgtgc tgtgtagata gttctactcg gaaaaagagt ggaaatttat 1200  
 taamatcaga aagtatgaga tctgtttatg ttaagggaaa tccaaattcc 1250  
 caattttttt tgggtttttt aggaagagat gttgtggtta aaagtgttag 1300  
 tatcaaatg ataatttact tgtagtcttt catgattaca ccaatgtatt 1350  
 ctagaatatg ttaggtctta ggaaattgtg gttaatttc tgacttttac 1400  
 aggttaagtgc aaaggagaag tgggtctcatg aaatgtctta atgtataata 1450  
 acattttact tcaagctcca tccagaatgga acgagtcttg agtaatcagg 1500  
 aagtatatct atagatcttt gatattgttt cataaataatt tgaagtctaa 1550  
 aagactgcat ttttaacaa gttagtatta atggtgtggt ccaactagca 1600  
 aaaagatatt tgattatctt aaaaattgtt aaatacctgt ttcattgaat 1650  
 tctcagatat tgtaacagca acttgtcaaa cctaagcata ttggaatatg 1700  
 atctccata atttgaatt gaaatcgtat tgtgtggttc tgcataattct 1750  
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 taaaagaaag taatggaag 1819

<210> 36  
 <211> 204  
 <212> PRT  
 <213> Homo sapiens

<100> 36  
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 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile  
 20 25 30  
 Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val  
 35 40 45  
 Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala  
 50 55 60  
 Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu  
 65 70 75  
 Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe  
 80 85 90  
 Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly  
 95 100 105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn
				110					115					120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn
				125					130					135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser
				140					145					150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val
				155					160					165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu
				170					175					180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp
				185					190					195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu						
				200										

<110> 37  
 <111> 330  
 <112> DNA  
 <113> Homo sapiens

<110>  
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 <112> 20, 35, 61, 83, 106, 130, 133, 137, 232, 260, 336  
 <113> unknown base

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 taghontgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150  
 aatagggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaccccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgacacactn gtgctcgcaa tgtgctccaa tcataggaga atatgctgga 300  
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 <112> DNA  
 <113> Homo sapiens

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 <112> 27

<223> unknown base

<400> 38

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tttttgactt ttacaggtaa gtgcbaagga gaagtgggtt catgaaatgt 200  
ctaatgtat aataacattt accttcagcc tcccatcaga atggaacgag 250  
tttgagtaa cccaggaagt atatttatat gatcttgata cctgtttata 300  
ttatttgaag cctaaaagac tgcattttta aacaagttag tattaatgag 350  
ttgcccacg tagcaaaaag atatttgatt atcttaaaaa ttgtcaata 400  
cagtttccat gaaagtcttc agtattgtaa cagcaacttg ccaaacctaa 450  
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtt 500  
gttgaaatg gcaatcttat gtgtgttgaa ggacacagta agagaccbaa 550  
gttgtcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<215>

<216> unsure

<217> 64-85, 206

<218> unknown base

<400> 39

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ctgttggcaa caatcacggc caagtgaact cgcbaatgac atcccagaga 150  
aatccataaac tgcctgtgggt cccgaagtgt taacccaaat gacacctgtc 200  
tggctngctg tgttaaaagt gaccactcgt gctcgcacat tgcctcaact 250  
ataagagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<215>

<223> Synthetic oligonucleotide probe

<400> 40  
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<210> 41  
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<213> Artificial Sequence

<214>  
<215> Synthetic oligonucleotide probe

<400> 41  
caggaatctgc tggagagg 18

<210> 42  
<211> 24  
<212> DNA  
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<214>  
<215> Synthetic oligonucleotide probe

<400> 41  
caggaatctcac taggattctgc gggg 24

<210> 43  
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<212> DNA  
<213> Artificial Sequence

<214>  
<215> Synthetic oligonucleotide probe

<400> 43  
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<210> 44  
<211> 2061  
<212> DNA  
<213> Homo sapiens

<400> 44  
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gacgtcttcag tctgagggac ctgtctgcac tgaggagagc agctgccaca 150  
cgggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200  
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 <211> 359  
 <212> P&T  
 <213> Homo sapiens

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 Gln Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Phe Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150  
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val  
 155 160 165  
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala  
 170 175 180  
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys  
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<110> 46

<111> 15

<112> DNA

<113> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<400> 46

aggactgtgt cctcatgg 18

<110> 47

<111> 15

<112> DNA

<113> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<400> 47

tttccagcgc caattctc 18

<110> 48

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 48  
attctatgga ctgtgataga cac 23

<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 49  
aaattatggt gtcttcagtg gctg 24

<211> 10  
<212> 48  
<213> DNA  
<214> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 50  
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<211> 11  
<212> 2181  
<213> DNA  
<214> Homo sapiens

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02100 52  
 02110 321  
 02120 PRT  
 02130 Homo sapiens

04000 52  
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr  
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 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
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 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
 50 55 60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
 65 70 75  
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
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 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
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 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
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 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
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 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
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 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
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 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
 170 175 180  
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
 185 190 195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	200	205	210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	215	220	225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	230	235	240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	245	250	255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	260	265	270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	275	280	285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	290	295	300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	305	310	315
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

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<410> 54

<411> 21

<412> DNA

<413> Artificial Sequence

<420>

<423> Synthetic oligonucleotide probe

<400> 54

gttcgaagac atcccaacaa g 21

<410> 55

<411> 14

<412> LNA

<413> Artificial Sequence

<420>

<423> Synthetic oligonucleotide probe

<400> 55

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<400> 56

<400> 24

<400> DNA

<400> Artificial Sequence

<400>

<400> Synthetic oligonucleotide probe

<400> 56

agaaatatc agcagctggt ttac 24

<400> 57

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<400> 57

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<400> 58

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<400> DNA

<400> Homo sapiens

<400> 58

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ccagctggcc cggaggtccgt cggaggggac cgggcggccc ggagccaagg 150

aggaactgag cgggggaagc cccgggtccg gggatcggga tgcacctcct 200

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tctacaataa cttgactgag gaacagaagg gcggagtggc ctttgcttcc 450

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 aatttgtgac aaaggattgt gaagagcttc ccatcttcat gatgttatga 2050  
 ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100



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 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu  
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<112> DNA

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Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
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Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
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Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Gln	
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Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
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Gln Gln Gly Pro	His His Arg His Ile	Leu Lys Leu Leu Pro	Ser
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Met Glu Ala Thr	Gly Gly Glu Lys Ser	Ser Thr Pro Ile Lys	Gly
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Pro Lys Arg Gly	His Pro Arg Gln Asn	Leu His Lys His Phe	Asp
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Ile Asn Glu His	Leu Pro Trp Met Ile	Val Leu Phe Leu Leu	Leu
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395		400	405
Lys Trp Ile Tyr	Tyr Cys Asn Gly His	Gly Ile Asp Ile Leu	Lys
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425		430	435
Phe Leu Cys Asn	Ala Ser Glu Arg Glu	Val Ala Ala Phe Ser	Asn
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Gly Tyr Thr Ala	Asp His Glu Arg Ala	Tyr Ala Ala Leu Gln	His
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Trp Thr Ile Arg	Gly Pro Glu Ala Ser	Leu Ala Gln Leu Ile	Ser
470		475	480
Ala Leu Arg Gln	His Arg Arg Asn Asp	Val Val Glu Lys Ile	Arg
485		490	495
Gly Leu Met Glu	Asp Thr Thr Gln Leu	Glu Thr Asp Lys Leu	Ala
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Leu Pro Met Ser	Pro Ser Pro Leu Ser	Pro Ser Pro Ile Pro	Ser
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Pro Asn Ala Lys	Leu Glu Asn Ser Ala	Leu Leu Thr Val Glu	Pro
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Ser Pro Gln Asp	Lys Asn Lys Gly Phe	Phe Val Asp Glu Ser	Glu
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Pro Leu Leu Arg	Cys Asp Ser Thr Ser	Ser Gly Ser Ser Ala	Leu
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<112> DNA

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Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile

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Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Gln
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Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala

	335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala	350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr	365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr	380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val	395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe	410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg	425	430	435
Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp	440	445	450

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<211> 74

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<221> Synthetic oligonucleotide probe

<400> 71

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<210> 71

<211> 74

<212> DNA

<213> Artificial Sequence

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<221> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gata 24

<210> 71

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<213> Artificial Sequence

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<400> 72

ngttcaatgc agaaatgata cagcctgtgt gcctgcccc aaatctgaagag 50

<10> 73

<11> 3305

<12> DNA

<13> Homo sapiens

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<111> 715

<112> PRT

<113> Homo sapiens

<400> 74

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Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala
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Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp
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Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu
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Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile
				80				85					90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp
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Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly
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His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	135	139	145
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	145	149	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	201	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Glu	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405



Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln  
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro  
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile  
725 730 735

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<221> unsure

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ctaccaggga agttttgcaga aacagtgcac ggaagggcag ganttcctgg 150

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gcagccttga taactggnt ntggctgcac nttaatgctn tgatatgggt 400

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gagacccctg caccattccc atntccatcc aag 483

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<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 76

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<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<221>

<221> Synthetic oligonucleotide probe

<221> 78

caatagratg tgaagggc 18

<221> 78

<221> 18

<221> DNA

<221> Artificial Sequence

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<221> 78

taactgacg atgggcac 18

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aaaggacac ctcccttc 18

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ctctagactg gtctccagtc cctccc 26

<221> 81

<221> 24

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 85

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Thr	Ser	Met	Pro	Glu	Ala	Thr	Ala	Ala	Glu	Thr	Thr	Lys	Pro	Ser
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Asn	Ser	Ala	Leu	Gln	Pro	Thr	Ala	Gly	Leu	Leu	Val	Val	Leu	Leu
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4213 Artificial Sequence

4220  
4223 Synthetic oligonucleotide probe

4300 86  
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4310 87  
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4313 Artificial Sequence

4320  
4323 Synthetic oligonucleotide probe

4400 87  
ggtagagatg tagaagggca agcaagacc 29

4410 88  
4411 51  
4412 DNA  
4413 Artificial Sequence

4420  
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4400 88  
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4510 89  
4511 2956  
4512 DNA  
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 ttaaggaaa cctttattaa tcaogtatgg ttcacagata attctctttt 4300  
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 cactaactca gcttctcctc acgagctctg tattccaaga aaatcaaaat 4500  
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 <211> 412  
 <212> PRT  
 <213> Homo sapiens

<4000> 90  
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 Gly Gly Arg Trp Gly Ala Arg Ala Gln Gln Ala Ala Ala Ala  
 35 40 45



Ala	Asp	Gly	Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro			
				53					55					59			
His	Ser	Lys	His	Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile			
				65					70					75			
Gln	Ser	Ala	Ala	His	Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly			
				80					85					90			
His	Cys	Gln	Arg	Leu	Gln	Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys			
				95					100					105			
Tyr	Asn	Ser	Met	Glu	Asp	Ala	Lys	Val	Tyr	Val	Ala	Lys	Val	Asp			
				110					115					120			
Cys	Thr	Ala	His	Ser	Asp	Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly			
				125					130					135			
Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys			
				140					145					150			
Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	Glu	Asn	Trp	Met	Leu			
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Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	Pro	Glu	Val	Glu			
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Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser			
				185					190					195			
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile			
				200					205					210			
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Tys	Lys	Ala	Leu	Ala	Pro			
				215					220					225			
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val			
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Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser			
				245					250					255			
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp			
				260					265					270			
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser			
				275					280					285			
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly			
				290					295					300			
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala			
				305					310					315			
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn			
				320					325					330			

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe  
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp  
350 355 360

Ile Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys  
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys  
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly  
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu  
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His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu  
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<210>

<213> Synthetic oligonucleotide probe

<210> 31

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<210> 37

<211> 41

<212> DNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<210> 31

ccagagcaac acactctaca g 21

<210> 33

<211> 34

<212> DNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<210> 37

aagtgatcgc cttgtgcaac gtgc 24

<210> 34

<211> 23

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4221  
4222 Synthetic oligonucleotide probe

4401 94  
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4410 95  
4411 44  
4412 DNA  
4413 Artificial Sequence

4420  
4421 Synthetic oligonucleotide probe

4400 95  
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4410 96  
4411 1016  
4412 DNA  
4413 Homo sapiens

4400 96  
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4210: 97  
 4211: 277  
 4212: PRT  
 4213: Homo sapiens

4403: 97  
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 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
 65 70 75  
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys  
 80 85 90  
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu  
 95 100 105  
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 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile  
 125 130 135  
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala  
 140 145 150  
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu  
 155 160 165  
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly  
 170 175 180  
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Leu  
 185 190 195  
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn	215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser	230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly	245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys	260	265	270
Glu Phe Ile Lys Lys Lys Lys	275		

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggtac 200  
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 <312> PFT  
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 20 25 30

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Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Asp	Pro		95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315



Val	Pro	Gly	Tyr	Leu	Ser	Ser	Pro	Gln	Ser	Ile	Thr	Asp	Thr	Cys	330	335	336
Leu	Tyr	Ile	Phe	Thr	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Ala	Ala	338	341	342
Arg	Ile	Ser	His	Leu	Lys	Ile	Leu	Gln	Cys	Gln	Gly	Phe	Tyr	Gln	350	351	360
Leu	Cys	Gly	Val	His	Gln	Glu	Asp	Val	Ile	Tyr	Leu	Ala	Leu	Pro	361	370	371
Leu	Tyr	His	Met	Ser	Gly	Ser	Leu	Leu	Gly	Ile	Val	Gly	Cys	Met	370	381	382
Gly	Ile	Gly	Ala	Thr	Val	Val	Leu	Lys	Ser	Lys	Phe	Ser	Ala	Gly	395	400	401
Gln	Phe	Trp	Glu	Asp	Cys	Gln	Gln	His	Arg	Val	Thr	Val	Phe	Gln	410	411	420
Tyr	Ile	Gly	Glu	Leu	Cys	Arg	Tyr	Leu	Val	Asn	Gln	Pro	Pro	Ser	415	430	431
Lys	Ala	Glu	Arg	Gly	His	Lys	Val	Arg	Leu	Ala	Val	Gly	Ser	Gly	440	445	450
Leu	Arg	Pro	Asp	Thr	Trp	Glu	Arg	Phe	Val	Arg	Arg	Phe	Gly	Pro	451	460	465
Leu	Gln	Val	Leu	Glu	Thr	Tyr	Gly	Leu	Thr	Glu	Gly	Asn	Val	Ala	470	475	480
Thr	Ile	Asn	Tyr	Thr	Gly	Gln	Arg	Gly	Ala	Val	Gly	Arg	Ala	Ser	485	490	495
Trp	Leu	Tyr	Lys	His	Ile	Phe	Pro	Phe	Ser	Leu	Ile	Arg	Tyr	Asp	501	505	510
Val	Thr	Thr	Gly	Glu	Pro	Ile	Arg	Asp	Pro	Gln	Gly	His	Cys	Met	515	520	521
Ala	Thr	Ser	Pro	Gly	Glu	Pro	Gly	Leu	Leu	Val	Ala	Pro	Val	Ser	530	535	540
Gln	Gln	Ser	Pro	Phe	Leu	Gly	Tyr	Ala	Gly	Gly	Pro	Glu	Leu	Ala	541	550	551
Gln	Gly	Lys	Leu	Leu	Lys	Asp	Val	Phe	Arg	Pro	Gly	Asp	Val	Phe	560	561	570
Phe	Asn	Thr	Gly	Asp	Leu	Leu	Val	Cys	Asp	Asp	Gln	Gly	Phe	Leu	575	580	581
Arg	Phe	His	Asp	Arg	Thr	Gly	Asp	Thr	Phe	Arg	Trp	Lys	Gly	Glu	590	595	600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp	605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His	620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His	635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu	650	655	655
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu	665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn	680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu	695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr	710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile	725	730	

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<110> 104  
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<223>  
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<100> 104  
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<110> 105  
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<223>  
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\*410\* 106  
\*411\* 1:  
\*412\* DNA  
\*413\* Artificial Sequence

\*420\*  
\*423\* Synthetic oligonucleotide probe

\*400\* 106  
atccattcca ggggacac 18

\*410\* 107  
\*411\* 4:  
\*412\* DNA  
\*413\* Artificial Sequence

\*420\*  
\*423\* Synthetic oligonucleotide probe

\*400\* 107  
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\*410\* 108  
\*411\* 2979  
\*412\* DNA  
\*413\* Homo sapiens

\*400\* 108  
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0210 109  
 0211 515  
 0212 PBT  
 0213 Homo sapiens

0000 109  
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 35 40 45  
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Gln His Leu Arg Ile Cys  
 50 55 60  
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Gln Met Glu Asp Lys Leu  
 65 70 75  
 Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu Thr  
 80 85 90  
 Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe  
 95 100 105  
 Asp Glu Phe Phe Arg Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu  
 110 115 120  
 Asn Asp Met Phe Val Arg Thr Tyr Gly Met Leu Tyr Met Gln Asn  
 125 130 135  
 Ser Glu Val Phe Gln Asp Leu Phe Thr Glu Leu Lys Arg Tyr Tyr  
 140 145 150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp		
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Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe		
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Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg		
515	520	525
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4210 113  
4211 4649  
4212 DNA  
4213 Homo sapiens

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 35 40 45  
 Trp Gly Gln Ala Leu Glu Gln Glu Glu Glu Gly Ala Leu Leu Ala  
 50 55 60  
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
 65 70 75  
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 80 85 90  
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
 95 100 105  
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro  
 110 115 120  
 Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln  
 125 130 135  
 Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro  
 140 145 150

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	155	160	161
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln	425	430	435

Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu  
440 445 450

Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr  
455 460 465

Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly  
470 475 480

Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe  
485 490 495

Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr  
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Gly Ile Gln Glu Ser  
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<230>

<231> unsure

<232> 33

<233> unknown base

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egg 53

4210 - 118

4211 - 2260

4212 - DNA

4213 - Homo sapiens

4220 -

4221 - unsure

4222 - 2009, 2026, 2033, 2055, 2074, 2078, 2086

4223 - unknown base

4310 - 118

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aactcagatg tctgaataca cagggaagct acaagtgtt ttgcctcagt 500

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cggaaactga atatctcagt ggaagatctg actgtataga tataaatgaa 800

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 <213> Homo sapiens

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Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
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Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
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Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
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Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
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Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
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Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
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Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
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Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	



Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro  
305 310 315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly  
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys  
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<210> 121  
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<221> Synthetic oligonucleotide probe

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<210> 122  
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<210> 123  
<211> 1199  
<212> DNA  
<213> Homo sapiens

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ggcagagtgg cagggacgac gccacagaatg ggagctgact gatatggttg 150  
tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200  
ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcctga 250

gotggaaagg gtgaaaagaa gatgocclaga gaatggcaat ttaaaagaaa 300  
 aagatataact tgttttgccc cttgaacotga ccgacactgg ttcccatgaa 350  
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 <212> PET  
 <213> Homo sapiens

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 35 40 45  
 Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu  
 50 55 60

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	155	160	165
Gly	Leu	Arg	Thr	Gln	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	275	280	285

Thr Lys His Asp

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<110> 1\*

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<400> 125

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4210 126

4211 19

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 126

ctgtgaatag cctcctggg 19

4210 127

4211 19

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 127

cttttcaagg cactggaggg 20

4210 128

4211 14

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 128

ctgttagaat ccaagctggg atcc 24

4210 129

4211 13

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 129

gagagctgc atccacacca ctc 23

4210 130

4211 46

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 130

acctgacgct actatggggc gactggcagg gacgacgcc agaattg 46

0210 • 131  
0211 • 2365  
0212 • DNA  
0213 • Homo sapiens

0400 • 131  
ctggacgtggg caccggccatc agctgttcgc ggcgtcttctc ctccaggtgg 50  
ggcaggggggt cggggctggg ggagcatgtg ctgggacagg acagcatcct 100  
caatcaatcc aacagcatat cgggttgcat cttctacaca ctacagctat 150  
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 <212> PRT  
 <213> Homo sapiens

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 Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys  
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Ile	Thr	Thr	Tyr	Ala	Ile	Asn	Val	Ser	Leu	Met	Trp	Leu	Ser	Phe	
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Arg	Lys	Val	Gln	Glu	Pro	Gln	Gly	Lys	Ala	Lys	Arg	His	Gly	Asp	
				50					55					60	
Thr	Val	Pro	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Val	Arg	Arg	Gln	
				65					70					75	
Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	
				80					85					90	
Leu	Thr	Ala	Ala	His	Cys	Phe	Gln	Lys	Ala	Ala	Ala	Thr	Glu	Leu	
				95					100					105	
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	
				110					115					120	
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	
				125					130					135	
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	
				140					145					150	
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	
				155					160					165	
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	
				170					175					180	
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	
				185					190					195	
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	
				200					205					210	
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	
				215					220					225	
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	
				230					235					240	
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Gln	Pro	Asp	Gly	His	Trp	
				245					250					255	
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	
				260					265					270	
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	
				275					280					285	
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	
				290					295					300	
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	
				305					310					315	

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp
				320					325					330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly
				335					340					345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys
				350					355					360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly
				365					370					375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly
				380					385					390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu
				395					400					405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys
				410					415					420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp
				425					430					435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln
				440					445					450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu
				455					460					465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met
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Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu
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Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu
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Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg
				515					520					525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser
				530					535					540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu
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Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser
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 (C11) 24  
 (C12) DNA



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<210> 134

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 136

<211> 1093

<212> DNA

<213> Homo sapiens

<400> 136

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ggggcagcct tccaccacgg ggagcccaga tgcagccgc ctccacaggaa 150

catgcttcgt cggcgggggca gccctggcat ggtgttgcac gtgggtgcag 200

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02110 316  
02110 PRT  
02130 Homo sapiens

02200  
02210 unsure  
02210 233  
02230 unknown amino acid

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20 25 30  
Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp  
35 40 45  
Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu  
50 55 60  
Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu  
65 70 75  
Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala  
80 85 90  
Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala  
95 100 105  
Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe  
110 115 120  
Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser  
125 130 135  
Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu  
140 145 150  
Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys  
155 160 165  
Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp  
170 175 180  
Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met  
185 190 195  
Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val  
200 205 210  
Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro  
215 220 225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln
				230					235					240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu
				245					250					255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys
				260					265					270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala
				275					280					285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln
				290					295					300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
				305					310					315

Ala

<210> 133  
 <211> 34  
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 <213> Artificial Sequence

<216>  
 <217> Synthetic oligonucleotide probe

<401> 139  
 atggcaccgc tcaacctcat ctgg 24

<210> 139  
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<216>  
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<401> 139  
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<210> 140  
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 <212> DNA  
 <213> Artificial Sequence

<216>  
 <217> Synthetic oligonucleotide probe

<401> 140  
 ggcacacagta tactgaccac 20

<210> 141  
 <211> 24

4212 - DNA  
4213 - Artificial Sequence

4221 -  
4223 - Synthetic oligonucleotide probe

4400 - 141  
tgaaacag gcagctgtg gtgc 24

4210 - 142  
4211 - 24  
4212 - DNA  
4213 - Artificial Sequence

4221 -  
4223 - Synthetic oligonucleotide probe

4400 - 142  
tgaaagaaga gggctgtgat gtgc 24

4211 - 143  
4212 - 45  
4213 - DNA  
4214 - Artificial Sequence

4221 -  
4223 - Synthetic oligonucleotide probe

4400 - 143  
caactgacag acaccaacaa gctggtgcac agtttcaccg aaggc 45

4210 - 144  
4211 - 2336  
4212 - DNA  
4213 - Homo sapiens

4221 -  
4222 - unsure  
4223 - 1630, 1673  
4224 - unknown base

4400 - 144  
ttcgtgaccc ttgagaaaag agttggtggg aaatgtgcc cgtcttctaa 50  
gaagggggag tcttgaaact gtctgaagcc ctgtctcgta agccttgaac 100  
taagtctcta aatctatgaa gtctagggac ctctgctgc ttctgtaggg 150  
actctcttcc ttgcttcaga aacatgagcc tttcttctgt gaacgcggtc 200  
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ggctccttat ttcactccac tcacaaacat aacaatggc agcccatttg 400

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 gcagctacca ttgaataaat acctatctg gatttt 1450

<210> 145  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<210> 145  
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 Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu  
 20 25 30  
 Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly  
 35 40 45  
 Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly  
 50 55 60  
 Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile  
 65 70 75  
 Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln  
 80 85 90  
 Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile  
 95 100 105  
 Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro  
 110 115 120  
 Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg  
 125 130 135  
 Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn  
 140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys  
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His  
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys  
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu  
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<230> 146

ctttcccttgc ttcagcaaca tgaggc 26

<240> 147

<241> 25

<242> DNA

<243> Artificial Sequence

<250>

<251> Synthetic oligonucleotide probe

<260> 147

ggcctagagca ggaggaatga tgagc 25

<270> 148

<271> 49

<272> DNA

<273> Artificial Sequence

<280>

<281> Synthetic oligonucleotide probe

<290> 148

gtggaagcgc gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<300> 149

<301> 2196

<302> DNA

<303> Homo sapiens

<400> 149

aataaaagctt ccttaatgtt gtatatgtct ttgaagtaca tccgtgcatt 50



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 cagagatgac tggctacccc gccctggccc cagcctcacg gggctcagtc 200  
 tctttttctc tttggctgca ccaggacgga gcctggaggt cacagtabct 250  
 gccaccccca acgtcccca tggctctgac gcccgccctg cctgcacccc 300  
 caactccctg tacacagtga accacaaaac gttctccctg aactggacct 350  
 accaggagtg caacaaactg cctgaggaga tgttccctca gttccgcatg 400  
 aagatcatta acctgaagct ggagcgggtt caagaccccg tggagttctc 450  
 agggaaaccc agcaagtaac atgtgtcggc gatgctgaga aacgtgcagc 500  
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 caacgtggcc atggcaagat ccatctgcag gtctcctgga aagagccccc 600  
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gtccaggtta gggggccatg ttccccagcg gggaccacc aacagaggcc 1550  
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 ataaggggag gcttgggac ctgagctgac aatgcagcc ctgtccctc 1850  
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 agtgacaat tgtaggccag gcacagtggc ccagctctt aatccagca 1950  
 cctggggagg ccaaggggg tggattacct ccctctgtt agtagaaatg 2000  
 tggaaaacc cactctact aaaaatcaa gaattagctg ggggtgggtg 2050  
 ggtctgctg taatccagc tatttgggag gctgaggcag gagaatcgct 2100  
 tgagccggg aagtagaggt tgcagtgaac tgatatagtg atagtgcac 2150  
 tgcattcag cctgggtgac atagagagac tccctctcaa aaaaaa 2196

<110> 150  
 <111> 215  
 <112> PRT  
 <113> Homo sapiens

<100> 150  
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 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met  
 20 25 30  
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
 35 40 45  
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
 50 55 60  
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
 65 70 75  
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
 80 85 90  
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
 95 100 105  
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu

110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<310> 151  
 <311> 514  
 <312> DNA  
 <313> Homo sapiens

<320>  
 <321> unsure  
 <322> 143, 133  
 <323> unknown base

<400> 151  
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 tctcctcttg tagttctcgc cccctcaaat cactttctcc cttagccac 100  
 ccaactaaca tctcagttctc tgaataatgca cagagatgac tggctacctc 150  
 ggcctgcctt cagcctcacc gggctcagtc tttttttctc ttgggtgcca 200  
 ccaggcaggga gcatggaggt ccacagtacc tgnccacct caactctctc 250  
 aatggctctg accccacct ggcctgcctt tcaactcctg ctacacagtg 300  
 aacacaaaac agttctcctt gaactggact taccaggagt gcaacaactg 350  
 ctctgaggag agttctctcc agttccgcat gaagatcatt aactgaagc 400  
 tggagcggtt tcaagacgcg gtggagttct cagggaaccc cagcaagtac 450  
 catgtgtcgg tgatgtgag aaactgacag ccggaggatg aggggattta 500  
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
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gaggtacaca taactgccac cctcaacgtc ctcaatgggt ttgaagcccg 100  
actccatgga accttcaact cccgtacac agtgaaccac aaacagttct 150  
ccttgaaatg gatttaccag gagtgcacaa actggctctg aggagatggt 200  
cttcacgttc ccgcattgga gatcatttaa cctgaaagct ggaagcgggt 250  
ttcagagacc gcttggaagt ttctcagga accccagcaa gtacgatgtg 300  
tgggtgatga tgagaaaagt gcagccggag gatgagggga ttacaactg 350  
taaatatg aacccccc 363

<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
gcacgtttct cagcatcacc gac 23

<210> 155  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 155

cgootgcoot gacottcaa ctctgtctac acagtgaann acaaacagtt 50

<210> 156

<211> 2630

<212> DNA

<213> Homo sapiens

<400> 156

tgggggagac gtgtacacac atgggcoctcc acctccggcc ctaccgtgtg 50

gggtgtctcc cggatggcct cctgttccctc ctgtctgtgc taatgtctgt 100

cggggaccca ggcctccggg cgggaagtca ccccccagtg gtgtcgggtcc 150

ctgttgattt gggtaaccaa ctggaagcca agctggacaa ggcgacagtg 200

gtgtactacc ctgtctccaa gaagacggaa agtacttca caatctggct 250

aaactgggaa ctgtctgtgc ctgtccatcat tgaactgtgg attgacaata 300

tcaagctggc ttacaacaaa acatccaggg ccacccagtt cctgtatggc 350

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ccctctgagg ctggggctac acacggggtg aggatgtccg aggggctccc 500

tatgaactgg gcgagccccc aaatgaaaa gggtccctact tctgggcoct 550

cgcgagatg atcgaggaga tgtaccagct gtatgggggc cccgtggctc 600

tgggtgcccc cagtatgggc aacatgtaca cgtctactt tctgcagcgg 650

cagccgcagg cctgggaagg caagtatata cgggcocttc tgtcactggg 700

tgcgcctctg gggggcgtgg ccaagacccct ggcgcctctg gcttcaggag 750

acacccaccc gatccagtc atcgggcccc tgaagatccg ggagccagcag 800

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cgggaggaca cagaagggtt ggttggaagcc acgatgcac ctggcgtgca 1000

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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

0110 157  
0110 412  
0112 PRT  
0113 Homo Sapien

0400 157  
Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp  
1 5 10 15  
Gly Leu Leu Phe Leu Leu Leu Leu Leu Met Leu Leu Ala Asp Pro  
20 25 30  
Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly  
35 40 45  
Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val  
50 55 60  
Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile  
65 70 75  
Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp  
80 85 90  
Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr  
95 100 105  
Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys  
110 115 120  
Thr Phe Ser Leu Glu Phe Leu Asp Pro Ser Lys Ser Ser Val Gly  
125 130 135  
Ser Tyr Phe His Thr Met Val Glu Ser Leu Val Gly Trp Gly Tyr  
140 145 150  
Thr Arg Gly Glu Asp Val Arg Gly Ala Pro Tyr Asp Trp Arg Arg  
155 160 165  
Ala Pro Asn Glu Asn Gly Pro Tyr Phe Leu Ala Leu Arg Glu Met  
170 175 180  
Ile Glu Glu Met Tyr Gln Leu Tyr Gly Gly Pro Val Val Leu Val  
185 190 195  
Ala His Ser Met Gly Asn Met Tyr Thr Leu Tyr Phe Leu Gln Arg  
200 205 210  
Gln Pro Gln Ala Trp Lys Asp Lys Tyr Ile Arg Ala Phe Val Ser  
215 220 225  
Leu Gly Ala Pro Trp Gly Gly Val Ala Lys Thr Leu Arg Val Leu  
230 235 240  
Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys

245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln Thr	
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe Gln	
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr Glu	
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His Cys	
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr Glu	
335	340	345
Ser Pro Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly Asp	
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp Gln	
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly Ser	
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr Leu	
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<110> 158  
 <111> 73  
 <112> DNA  
 <113> Artificial Sequence

<121>  
 <123> Synthetic oligonucleotide probe

<400> 158  
 atgggactac acacggggtg agg 23

<210> 159  
 <211> 74  
 <212> DNA  
 <213> Artificial Sequence

<221>  
 <223> Synthetic oligonucleotide probe

<400> 159  
 ggtggcggctg cagaaagtag agcg 24



4210 - 160  
4211 - 45  
4212 - DNA  
4213 - Artificial Sequence

4220 -  
4223 - Synthetic oligonucleotide probe

4408 - 160  
gccccaaatg aaaaaggggc ctacttcctg gccctccggc agatg 45

4210 - 161  
4211 - 1012  
4212 - DNA  
4213 - Homo sapiens

4408 - 161  
gggacgggtg gggggacggc gggggggggc gacggggg gacggggac 50  
atcgagagcg gggcctaagg cgggggcaag ggggggggct ccttcgacct 100  
cccgcgcttc ctgacgcagc cgcaggtggc ggcgcgggcc gtgtgcttgg 150  
cttcggcctt gatcggttc cctgcacct atggcgaggc ctacagcaat 200  
gccccagat ctaagcagat gtactggctg cccaacggca acgaggatgc 250  
ctgcgcctat ggcagtgcca tgggggtgct ggcttcctg gcctgggct 300  
cttccttggc ggtcgacggc tatttcctcc agatcagcaa cgcacctgac 350  
agcagtcacc tggtcattgg cgacctgctc ctctcagctc ctgggacct 400  
ctcttgggtt gttgggttct gcttcctcac caaccagtcg gcagtcacca 450  
cccggaagga cgtgctggcg ggggcagact ctgtgagggc agccatcacc 500  
ctcagcttct cctccatctt cctctggggt gtgttggtct ccttggtcta 550  
ccatcgctac aaggctggcg tggacgact cctccagaat tgcctcgacc 600  
ccactccgga ccccaacact gctacggct cctaccagc tgcctctgtg 650  
gaaactacc aacagccacc ctccaccag aacggggaga ccacccaggg 700  
ctaccagcgg cccctgtgt aotgagtcgc ggttagcgtg ggaaggggga 750  
cagagagggc cctccctctt gccctggact ctccatcag cctcctggaa 800  
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 gcttcagctt ccccccggcc cgggtcagga cgtgggagcc gctattatct 1100  
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 cggcccatg gctccacagc ctgtctctgt ccgagtgtat tataaaatcg 1450  
 tggggagat gcccggctg ggatgctgt tggagacgga ataaatgtt 1500  
 tctcattcaa ag 151.

0010 - 162  
 0011 - 214  
 0012 - PRT  
 0013 - Homo sapiens

0010 - 162  
 Met Gly Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe  
 1 5 10 15  
 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala  
 20 25 30  
 Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly  
 35 40 45  
 Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val  
 50 55 60  
 Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly  
 65 70 75  
 Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala  
 80 85 90  
 Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val  
 95 100 105  
 Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe  
 110 115 120  
 Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro  
 125 130 135  
 Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr  
 140 145 150



<401> 166  
ccaggagggt catgggaaag tcc 23

<210> 167  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<401> 167  
ccaggagggt aagcagatgt actgctgttt caacggcaac gaggatgct 50

<210> 163  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 163  
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ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150  
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cagggtgaact caggcagtc gctgtgaact aatcgccact tctcccagga 350  
tcttacccgc cgggaatcta gtgccttcgg cagtgaacac gccaaagccc 400  
agaagatgct caaggagctc atcacagca ccgcctggg aaattactac 450  
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tgggttggtt ccgtacagc taagtgggc agggccaggt cctccggctg 750  
aaggggcttg accacctggc ctccagctgc ctgtggcacc tgcagggccc 800  
caaggacctc atgctcaaac tccgctcgga gtggacgctg gcagagtgcc 850  
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actacgaccc cttcgtgctc tccgtgcagc cggcggctct ccaggccctgt 1050  
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 aagtgggga agtctgact ccaggtctct tgcctcacc ctcctgcaca 3050  
 cctgggcccc cacagcccag acctcactg ggaggtgagc tcagctgccc 3100  
 ttctggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<110> 169  
 <111> 302  
 <112> PRT  
 <113> Homo sapiens

<400> 169  
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 1 5 10 15  
 Gly Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala  
 20 25 30  
 Cys Glu Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val  
 35 40 45  
 Pro Leu Phe Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly  
 50 55 60  
 Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val  
 65 70 75  
 Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn Arg His Phe  
 80 85 90  
 Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu

	45	100	105
Thr Ala Lys Ala	Gln Lys Met Leu Lys	Gln Leu Ile Thr Ser	Thr
	110	115	120
Arg Leu Gly Thr	Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe	Gly
	115	120	135
Glu Gly Pro Leu	Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile	Pro
	140	145	150
Glu His Arg Arg	Leu Met Leu Ser Pro	Gln Val Val Gln Ala	Leu
	155	160	165
Leu Val Glu Glu	Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala	Val
	170	175	180
Pro Tyr Arg Ala	Gln Tyr Glu Val Asp	Pro Glu Gly Leu Val	Ile
	185	190	195
Leu Glu Ala Ser	Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr	Leu
	200	205	210
Gly Cys Tyr Arg	Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu	Arg
	215	220	225
Leu Lys Gly Pro	Asp His Leu Ala Ser	Ser Cys Leu Trp His	Leu
	230	235	240
Gln Gly Pro Lys	Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp	Thr
	245	250	255
Leu Ala Glu Cys	Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala	Gly
	260	265	270
Pro Leu Glu Lys	Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser	Arg
	275	280	285
Gln Glu Pro Val	Val Glu Val Leu Ala	Ser Gly Ala Ile Met	Ala
	290	295	300
Val Val Trp Lys	Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe	Val
	305	310	315
Leu Ser Val Gln	Pro Val Val Phe Gln	Ala Cys Glu Val Asn	Leu
	320	325	330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr	Pro
	335	340	345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp	His
	350	355	360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe	Asp
	365	370	375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr	Gln

380										395					340				
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile					
				395					400					405					
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly					
				410					415					420					
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly					
				425					430					435					
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro					
				440					445					450					
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys					
				455					460					465					
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys					
				470					475					480					
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile					
				485					490					495					
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly					
				500					505					510					
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Leu	Gly	Val	Pro	Cys	Gly	Thr	Pro					
				515					520					525					
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro					
				530					535					540					
Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu					
				545					550					555					
His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly					
				560					565					570					
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu					
				575					580					585					
Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp					
				590					595					600					
Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Ile	Gln	Glu	Asp	Ser	Met					
				605					610					615					
Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln					
				620					625					630					
Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Ile	Lys	Val	Ser	Arg	Leu					
				635					640					645					
Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val					
				650					655					660					
Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val					



665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly		
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly		
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro		
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg		
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln		
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg		
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg		
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser		
785	790	795
Trp Ile Gln Gln Val Val Thr		
800		

0110 - 170  
 0111 - 1827  
 0112 - DNA  
 0113 - Homo sapiens

0400 - 170  
 gcaacccggg ccagtggaag atccagaaca ggaggtgtg tggcttgccg 50  
 atcttgagc cctacgcgca gaggatcccc gtggaggcca cggccgggat 100  
 caccatcaac ttcacctccc agatctccct caccgggccc ggtgtggggg 150  
 tgcactatgg ctgtgacaa cagtcggacc ctgtctctgg agagttcttc 200  
 tgtctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
 ccccaacggc ctggatgaga gaaactgggt ttgagagacc acattccagt 300  
 gcaagaggga cagcacatgc atctcactgc ccaaggtctg tgatggggcag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtaccagg aagggggtgc 400  
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 ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctgggatgag 500  
 gagaactgtg actgtggcct ccaggggccc tccagccgca ttgttggtgg 550

agatgtgttc tccaggggtg agtggccatg gcaggccagc ctccaggttc 630  
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 gacgtgttc ctgggcaagg tgtggcagaa ctggcgtgg ccaggagagg 750  
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 ggtccctggt tgtgcaaggc actcagtggc cgtcggttc tggcggggt 1150  
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 ccgcatcac aggtgtgata agctggatcc agcaagtgg gacctgagga 1250  
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 gcaatgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<240> 171

taacagctgc ccactgcttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<240> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA

<214> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 173

atgacctcca cggtagctgtg gacagtgttc ctgggcaagg tgtggcagaa 50

<214> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 174

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<214> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 175

aggaagagac acagagtcca ttcac 25

<214> 176

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 176

agtatgattt gcctgtgacc cagggcaggt ggacgatcca gaacaggagg 50

<214> 177

<211> 140

<212> DNA

<213> Homo sapiens

<400> 177

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ccacggcccg ggctccgtgc cgcacagttt tcattttcca ccttctctgc 100

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 tgggaatgt ccacttgatc ggtacagcc tcggagcgca cgtggccggg 750  
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 ggctgagca ttggtattca gatgctgtg ggccacattg acatctacc 950  
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 gccctccacc tctttgttga ctctctgtg aatcaggaca agccgagttt 1100  
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 gctgcgcgca gaaccgctgt aatagcattg gctacaatgc caagaaaatg 1200  
 aggaacaaga ggaacagcaa aatgtacctt aaaaacccgg caggcatgoc 1250  
 tttcagaggt aaccttcagt cctggagtg tccctgagga aggcctctaa 1300  
 taactctctc ttaataccat gctgcagagc agggcacatc ctagcccagg 1350  
 agaagtggcc agcacatcc aatcaaatcg ttgcaaatca gattacactg 1400  
 tgcctgtctt aggaaaggga atctttacaa aataaacagt gtggacccct 1450  
 aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa 1510

(210) 173  
 (211) 354  
 (212) PRT  
 (213) Homo sapiens

<400> 178

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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg	
				20					25					30	
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val	
				35					40					45	
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu	
				50					55					60	
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu	
				65					70					75	
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His	
				80					85					90	
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu	
				95					100					105	
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val	
				110					115					120	
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val	
				125					130					135	
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp	
				140					145					150	
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu	
				155					160					165	
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn	
				170					175					180	
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala	
				185					190					195	
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro	
				200					205					210	
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser	
				215					220					225	
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp	
				230					235					240	
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn	
				245					250					255	
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val	
				260					265					270	
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu	
				275					280					285	

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser  
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg  
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg  
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg  
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro  
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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 179

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<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 180

gcatatgcaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagcaga gttttgcctt ccag 44

<210> 182

<211> 3040

<212> DNA

<213> Homo sapiens

<400> 182

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actcagtgt gggcaacctg cgtctctcgc tacagatctt accccaggat 2150  
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 ggtctggaca ctccatcctt gcbaaacctc taccbaaaag tggccttaag 3050  
 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100  
 tgggcagaac ctgagggttt gcacccaca atccctcata cagggcctgg 3150  
 ctacaaaaaa gagggaaca aatgcttcta ctccatagct caggcattgc 3200  
 ccagtaagtt gaggtcaaaa ataaaggaat caccatctc 3240

<210> 153  
 <211> 713  
 <212> PRT  
 <213> Homo sapiens

<400> 153  
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 1 5 10 15  
 Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp  
 20 25 30  
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro  
 35 40 45  
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu  
 50 55 60  
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys  
 65 70 75  
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro  
 80 85 90  
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu  
 95 100 105  
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly  
 110 115 120  
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln  
 125 130 135  
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His  
 140 145 150  
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys  
 155 160 165  
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro  
 170 175 180  
 Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr

185	195	195
Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His 200 217		
Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp 215 228		
Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp 230 240		
Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro 245 255		
Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn 260 270		
Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val 275 285		
Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala 290 300		
Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys 305 315		
Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg 320 330		
Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala 335 345		
Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His 350 361		
Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr 365 375		
Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly 380 390		
Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg 395 405		
Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly 410 420		
Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr 425 435		
Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu 440 450		
Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys 455 465		
Leu Tyr Ala Ile Arg Thr Gln Glu Tyr Ser Ile Phe Ala Pro Leu		

473	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro Ser	
485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu Asp	
500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn Leu	
515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly Gly	
530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg Arg	
545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr Asn	
560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro Ser	
575	580	585
Ala Ala Pro Leu Gln Ala Leu Asp Gly	Gly Thr Gly Pro Ala Arg	
590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro Pro	
605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro Ala	
620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu Pro	
635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val	Val Gln Ala Leu Arg Gly	
650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser Pro	
665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp Asp	
680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro	Gly Val Trp Val Ala Glu	
695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr		
710		

<110> 1-4

<111> 2-3

<112> DNA

<113> Artificial Sequence

<200>

<223> Synthetic oligonucleotide probe

<400> 184  
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<400> 185  
<401> 18  
<402> DNA  
<403> Artificial Sequence

<400>  
<403> Synthetic oligonucleotide probe

<400> 185  
cttgggtcat tacagctg 18

<400> 186  
<401> 23  
<402> DNA  
<403> Artificial Sequence

<400>  
<403> Synthetic oligonucleotide probe

<400> 186  
gttccatagg agcagtcaca ctc 23

<400> 187  
<401> 23  
<402> DNA  
<403> Artificial Sequence

<400>  
<403> Synthetic oligonucleotide probe

<400> 187  
tgactgtatgc tgcacaatct cag 23

<400> 188  
<401> 45  
<402> DNA  
<403> Artificial Sequence

<400>  
<403> Synthetic oligonucleotide probe

<400> 188  
gggtatttgt tgctttggga cagacctgt ggcttaggct ctggc 45

<400> 189  
<401> 643  
<402> DNA  
<403> Homo sapiens

<400> 189  
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gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150  
 aataaaaacat cgcaccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
 tgcgggtggc actaactgtg acatctatga ccttttttat catcgacaaa 250  
 gccctcgaac catatattgt taccactgga ttggaagtcg ccgttatctt 300  
 atttttcata ctttttatgt tactcagaat tgcacgatta atgaagtggc 350  
 tattttggcc ttgccttgat attatcaact cactggtaac aacagtattc 400  
 atgctcctcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450  
 agttggctga ggggtgttgc cactctgac agcagtatgc tgtcttgccg 500  
 acggggccct tatttcgcg aagcttcgt ccaatcccag cggtccttac 550  
 cagaaaaagc ctgtgcctga aaaaaaagaa gttttgtaat tttatattac 600  
 ctttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650  
 aaaaaaaaaa aaa 663

<010> 190  
 <011> 192  
 <012> PRT  
 <013> Homo sapiens

<400> 190  
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 20 25 30  
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr  
 35 40 45  
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile  
 50 55 60  
 Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe  
 65 70 75  
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe  
 80 85 90  
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr  
 95 100 105  
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys  
 110 115 120  
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn  
 125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
 140 145 150

Val Leu

<210> 131  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> feature  
 <222> 7, 212, 234, 487  
 <223> unknown base

<400> 141  
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 tttagagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100  
 ctctgtgtgg gtctgcagac gogatggata acgtgcagcc gaaaataaaa 150  
 cctggcgcct tctgcttcag tctgaaagga caogtgaaga tctgcgggct 200  
 ggcactaacg gngacatcta tgacctttt tatnctgca caagcccttg 250  
 aacacatat tcttatcact ggatttgaag tcacgttat cttatttttc 300  
 atattttat atgtactcag acttgatoga ttaatgaagt ggttattttg 350  
 ggccttgcct gatattatca accactgggt aacaacagta ttcctgctca 400  
 tcttatctgt gttggcactg ataccagaaa ccacaacatt gacagtctgt 450  
 gggggggtgt ttgcacttgt gacagcagta tctgtnttg ccgac 495

<210> 142  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Synthetic oligonucleotide probe

<400> 142  
 cgttttcag aactactca ggcag 25

<210> 143  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Synthetic oligonucleotide probe

<400> 192

ccctccancaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgtg tgctgggtct gcagacggga tggataacgt 40

<210> 195

<211> 1-79

<212> DNA

<213> Homo sapien

<400> 195

cagccccggg cgcggggcga gtgcttgaga cggggctgca ggaaggagag 50

ggacgggcta ggttgggggc gccccgggg cccggcctg ggcattgggg 100

caatggcccc ggctgtgtgt ctgcctctgc tggcccagtg gctcctgggc 150

gcgcgggggc agctggcccc cgggccttcc acgttgcccc tcgggggggc 200

cggggcagag aacgggttag ttggggccac cccgggaccc gggacccctg 250

ccgagggcca cgcgcagggc ttggggctcg cctgggagcc tgccttgggc 300

tcgggggggc ggcgcggcaa cttcttgggc atggttagaca acctgcaggg 350

ggacttgggc cggggctact acctggagat gctgatcggg accccccgcg 400

agaagtcaca gattctcgtt gacactggaa gcagtaactt tgccttgggc 450

ggatccccgc acctctacat agacacgtac ttgacacag agaggtctag 500

caatccccgc tccagggtct ttgacgtcac agtgaagtac acacaaggaa 550

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aatacttctt ttcttgccaa cattggcact atttctgaat cagagaattt 650

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caatggccaa gccatcaagt tctctggaga cctctcttga ctccctgggt 750

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cttgcacctt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850

gaattgaacc aagtttgtat aaaggagaca tctgggtata cctattaag 900

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aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000  
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aaataattaa aaaaaaaact tcattctaa 1879

<210> 196  
<211> 513  
<212> PRT  
<213> Homo sapien

<400> 126  
Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Glu  
1 5 10 15  
Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr  
20 25 30  
Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro  
35 40 45  
Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu  
50 55 60



Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala	
				65					70					75	
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg	
				80					85					90	
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu	
				95					100					105	
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	
				110					115					120	
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	
				125					130					135	
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	
				140					145					150	
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Gln	Asp	Leu	Val	Thr	Ile	
				155					160					165	
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	
				170					175					180	
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	
				185					190					195	
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	
				200					205					210	
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	
				215					220					225	
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	
				230					235					240	
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	
				245					250					255	
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	
				260					265					270	
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	
				275					280					285	
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	
				290					295					300	
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	
				305					310					315	
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	
				320					325					330	
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	
				335					340					345	

Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile	350	355	360
Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile	365	370	375
Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn	380	385	390
Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu	395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp	410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu	425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr	440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu	455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly	470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg	485	490	495
Cys Glu Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser	500	505	510
Ser Leu Val Arg His Arg Trp Lys	515		

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

cgacgaagct acagattctc g 21

<210> 148

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

ggaaattgga ggccaaagc 19

42115 199  
42115 20  
42115 DNA  
42115 Artificial Sequence

42200  
42200 Synthetic oligonucleotide probe

44000 129  
ggatgtagcc agcaactgtg 20

42116 198  
42116 19  
42116 DNA  
42116 Artificial Sequence

42300  
42300 Synthetic oligonucleotide probe

44000 100  
ggcttggctc gttctcttc 19

42117 197  
42117 18  
42117 DNA  
42117 Artificial Sequence

42300  
42300 Synthetic oligonucleotide probe

44000 99  
gttctctgagc ctggatgg 18

42118 196  
42118 21  
42118 DNA  
42118 Artificial Sequence

42300  
42300 Synthetic oligonucleotide probe

44000 211  
gacaaagacta cctcagttgg tc 22

42119 193  
42119 24  
42119 DNA  
42119 Artificial Sequence

42300  
42300 Synthetic oligonucleotide probe

44000 205  
tgaagaaagag ttcagcacct gttg 24

42100 204

4211 - 47  
4212 - DNA  
4213 - Artificial Sequence

4220 -  
4221 - Synthetic oligonucleotide probe

4400 - 24  
gggtcgaagg gcttggaggt cacagtgaag tacacacaag gaagctg 47

4410 - 245  
4411 - 1439  
4412 - DNA  
4413 - Homo sapiens

4400 - 245  
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 gggcttgagg ocagggcoga ctgocgtaag atgggtgctg agaagttagt 1800  
 cagggcaggg cagctggtat cgaggtgooo catgggagta aggggaogoo 1850  
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 taaagoggtt tgacogocaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<240> 206  
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 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly  
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 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn  
 35 40 45  
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly  
 50 55 60  
 Ala Arg Val Val Leu Ala Cys Arg Ser Glu Glu Arg Gly Glu Ala  
 65 70 75

Ala	Ala	Phe	Asp	Leu	Arg	Gln	Glu	Ser	Gly	Asn	Asn	Glu	Val	Ile	
				80					85					90	
Phe	Met	Ala	Leu	Asp	Leu	Ala	Ser	Leu	Ala	Ser	Val	Arg	Ala	Phe	
				95					100					105	
Ala	Thr	Ala	Phe	Leu	Ser	Ser	Glu	Pro	Arg	Leu	Asp	Ile	Leu	Ile	
				110					115					120	
His	Asn	Ala	Gly	Ile	Ser	Ser	Cys	Gly	Arg	Thr	Arg	Glu	Ala	Phe	
				125					130					135	
Asn	Leu	Leu	Leu	Arg	Val	Asn	His	Ile	Gly	Pro	Phe	Leu	Leu	Thr	
				140					145					150	
His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	
				155					160					165	
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	
				170					175					180	
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	
				185					190					195	
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	
				200					205					210	
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	
				215					220					225	
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	
				230					235					240	
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	
				245					250					255	
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	
				260					265					270	
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	
				275					280					285	
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	
				290					295					300	
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	
				305					310					315	
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	
				320					325					330	
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	
				335					340					345	
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	
				350					355					360	

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln  
 365 370 375

Leu Ser

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 <112> DNA  
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<110>  
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<400> 107  
 attcatggcc ttggacttgg ccag 24

<110> 208  
 <111> 24  
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<110>  
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<400> 208  
 acctccagtgg cctccaagctg gttg 24

<110> 279  
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<110>  
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<400> 269  
 atttctgagc cctgagccac ggttggacat cctcatccac aatgc 45

<110> 210  
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<400> 210  
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<010> 111  
 <011> 985  
 <012> PRT  
 <013> Homo sapiens

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 Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro Ala Arg Met Ser  
 20 25 30  
 Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu  
 35 40 45  
 Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu  
 50 55 60  
 Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly  
 65 70 75  
 His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr  
 80 85 90  
 Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly  
 95 100 105  
 Ala Arg Leu Ser Val Ala Val Leu Arg Gln Asp Phe Gln Ile Gln  
 110 115 120  
 Pro Arg Asp Met Val Ala Val Val Gly Gln Gln Phe Thr Leu Glu  
 125 130 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Gln Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met	Glu	Arg	Ala	Thr	Gln	Glu	Pro	Ser	Glu	His	Gly	Pro	Trp	Thr	425	430	435
Leu	Glu	Gln	Leu	Arg	Ala	Thr	Leu	Lys	Arg	Pro	Glu	Val	Ile	Ala	440	445	450
Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Gly	Thr	Ala	Val		455	460	465
Cys	Ile	His	Arg	Arg	Arg	Arg	Ala	Arg	Val	His	Leu	Gly	Pro	Gly	470	475	480
Leu	Tyr	Arg	Tyr	Thr	Ser	Glu	Asp	Ala	Ile	Leu	Lys	His	Arg	Met	485	490	495
Asp	His	Ser	Asp	Ser	Gln	Trp	Leu	Ala	Asp	Thr	Trp	Arg	Ser	Thr	500	505	510
Ser	Gly	Ser	Arg	Asp	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Arg	515	520	525
Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu	530	535	540
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp	545	550	555
Thr	Ser	Thr	Phe	Tyr	Gly	Ser	Leu	Ile	Ala	Glu	Leu	Pro	Ser	Ser	560	565	570
Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu	575	580	585
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp	590	595	600
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu	605	610	615
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln	620	625	630
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu	635	640	645
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser	650	655	660
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala	665	670	675
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg	680	685	690
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr	695	700	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Gln	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Gln Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

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<211> Artificial Sequence

<220>  
<222> Synthetic oligonucleotide probe

<400> 112  
gaaaggacot acatgtgtgt ggcc 24

<211> 115  
<211> 24  
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<220>  
<222> Synthetic oligonucleotide probe

<400> 214  
actgacatto cagctgagcc acaa 24

<211> 214  
<211> 30  
<211> DNA  
<211> Artificial Sequence

<220>  
<222> Synthetic oligonucleotide probe

<400> 114  
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<210> 214  
<211> 1749  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1969, 1987  
<223> unknown base

<400> 214  
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ggcgggttcca aggggacact gtgtccctgc agtgcaccta cagggaagag 150  
ctgagggcac accggaagta ctgggtgcagg aagggtggga tctctctctc 200  
tcgtgtctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250  
agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

acctgttga acctcaccct gcaagacgct ggggagtact ggtgtggggc 350  
 cgaaaaaagg ggccccgatg agtcttact gatctctctg ttogtctctc 400  
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<110> 216

<111> 332

<112> PRT

<113> Homo sapiens

<400> 216

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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
			20					25					30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
			35					40					45	

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



50					55					60				
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Gln	Gly	Gln	Glu	Thr	Met
				65					70					75
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu
				80					85					90
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr
				95					100					105
Trp	Cys	Gly	Val	Gln	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile
				110					115					120
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser
				125					130					135
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala
				140					145					150
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu
				155					160					165
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Gln
				170					175					180
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr
				185					190					195
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro
				200					205					210
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala
				215					220					225
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg
				230					235					240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu
				245					250					255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His
				260					265					270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln
				275					280					285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys
				290					295					300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro
				305					310					315
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val
				320					325					330
Ser	Ala													

<210> 217  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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ccctgagtg cactacag gaag 24

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 218  
ctgtctccc ctgcttggt gtgg 24

<210> 219  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 219  
gggtgaggaa ggggtggatc ctctctctc gtgctctgg ccacac 47

<210> 220  
<211> 350  
<212> DNA  
<213> Homo sapiens

<400> 220  
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cagtggtgaaa gaaccagtgg ctctgctctg ttgcccaggc tagagtgtao 150  
tggcgtgata atagctcact gcagcctcag actcctggac ttgagaaatc 200  
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cctgttctct ctctctctgt gagtggacca cggaggctgg tgagctgctt 300  
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ccgcgggcac agaagccagg agcagggtc tcagaaggcg gtggtgcccc 400

gctgggataa tgttgttggc cctgggtctgt ctgctcagct gcttctacc 450  
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<210> 221  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<210> 221  
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 20 25 30  
 His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp  
 35 40 45  
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala  
 50 55 60  
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln  
 65 70 75  
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro  
 80 85 90  
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu  
 95 100 105  
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln  
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 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys  
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 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe  
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<210> 222  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 222  
gggatcatgt tggtagccct ggta 24

<210> 223  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 223  
gaaaggtaga cccagtcaga cag 23

<210> 224  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 224  
atgactctta cctccaaagt gaggccaagc tatacggtag ttgtg 45

<210> 225  
<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
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 ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcttc 2044

00100 216  
 00110 391  
 00120 PRT  
 00130 Homo sapiens

00000 216  
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 20 25 30  
 Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
 35 40 45  
 Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
 50 55 60  
 Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
 65 70 75  
 Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
 80 85 90  
 Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
 95 100 105  
 Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
 110 115 120  
 Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys  
 125 130 135  
 Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe  
 140 145 150  
 Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe  
 155 160 165  
 Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser  
 170 175 180  
 Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg  
 185 190 195  
 Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly  
 200 205 210  
 Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro

	215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly	230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu	245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu	260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg	275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser	290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe	305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe	320	325	330
His Thr Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val	335	340	345
His Leu His Thr Cys Arg	350		

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<211> 23

<212> RNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<210> 217

ggagcagctg caaatccac tgg 23

<211> 213

<212> RNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<210> 218

tggtgacaga ctgtttaaat tatcgcc 28

<211> 219

<212> RNA

<213> Artificial Sequence

<220>

4223 · Synthetic oligonucleotide probe

4410 · 219

tggttctctca agtgccgggca gtgccagcgg ctctgtggagt t 41

4210 · 210

4211 · 1155

4212 · DNA

4213 · Homo sapiens

4410 · 230

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cgatgattga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300

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 aaaaa 1355

00100 031  
 00110 093  
 00120 PRT  
 00130 Homo sapiens

00000 031  
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 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
 20 25 30  
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
 35 40 45  
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
 50 55 60  
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
 65 70 75  
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
 80 85 90  
 Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
 95 100 105  
 Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
 110 115 120  
 Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
 125 130 135  
 Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg  
 140 145 150  
 Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys  
 155 160 165  
 Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser  
 170 175 180  
 Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp  
 185 190 195  
 Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly  
 200 205 210

Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu
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				230					235					240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro
				245					250					255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr
				260					265					270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp
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				290										

<212> 232

<212> 24

<212> DNA

<212> Artificial Sequence

<212>

<212> Synthetic oligonucleotide probe

<212> 232

gcacgaactg tgatcatgatg ctgg 24

<212> 233

<212> 24

<212> DNA

<212> Artificial Sequence

<212>

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<212> 233

gtttctgaga ctacagagag gtgg 24

<212> 234

<212> 5'

<212> DNA

<212> Artificial Sequence

<212>

<212> Synthetic oligonucleotide probe

<212> 234

caacgtatga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<212> 235

<212> 1-47

<212> DNA

<212> Homo sapiens

<400> 235

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gttgggaaaag cggcagcccc cggcgcccco gcagccactt ctactacttc 100  
ctcccaagtc ctatctgctt ctccgtggag gccaggccgt gcagcatcga 150  
agacaggagg aactggagcc tcattggcgg gcccgggggg cgggcctcgg 200  
gcttaaatag gagctccggg ctctggctgg gacccgaccc ctggccggccg 250  
cgctcccgct gctcctggcg ggtgatggaa aaccccagcc cggccggccg 300  
cctgggcaag gccctctggg ctctcctcct ggccactctt ggcggccgg 350  
gccagcctct tgggggagag tccatctgtt ccggcagagc cccggccaaa 400  
tacagcatca ccttcacggg caagtggagc cagacggcct cccccaagca 450  
gtacccctg tccggcccco ctgggcagtg gtcttcgttg ctggggggcg 500  
cgcatagctc cgaactacag atgtggaggga agaaccagta cgtcagtaac 550  
gggtcggcg actttcgga gggcgcgag gctggggcg tgatgaaggga 600  
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cgcccgccgt ccccgagggo accgggcaga cgtcggggga gctggagggtg 700  
caggccaggc actcgtcgtt ctggttctg gtggccatcg tggccagccc 750  
cgaactggtt gtggcggtgg acagcctgga cctgtggac ggggaacgctt 800  
ggcgggaaac gggcgcgctg gacctgtacc cctacgacgc cgggacggac 850  
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ggtgaccgag ataaagtcct cctctccca gcaacccggc aactccttct 950  
actaccccg gctgaaggcc ctgcctccca tggccagggt gacactgctg 1000  
cggctggcac agagcccccag ggcccttcac cctcccgccc cagtcccgcc 1050  
caggcgggac aatgagattg tagacagcgc ctcagttcca gaaaacggcg 1100  
tgactgcca ggtctccctg tggctgtcct ggggactgtg cggaggccac 1150  
tgtgggaggc tgggaccaa gaggaggact cgtacgttc gggtcacgcc 1200  
cgccaaacac gggagccctt gccccgagct cgaagaagag gctgagtgcg 1250  
tccttgataa ctgggtctaa gaccagagcc ccgcagcccc tggggcccco 1300  
cggagccatg ggggtcggg ggctcctgt caggctcatg ctgcaggcgg 1350  
ccgagggcac agggggtttc ggcctgctcc tgaccgggt gaggcccgcg 1400

agaccatctc tgcactgaag ggcctctctg tggccggcac gggcattggg 1450  
 aaacagcctc ctcccttccc aaccttgctt cttaggggac ccctgtgtcc 1500  
 gctatgctct agctctctcc tcttgacgga taaagtcata cccaaggctc 1550  
 cagctactct aaattaatgc tctttataag ctattgctgc tccaggagat 1600  
 tgcctctcat cgtccagggg cctgggtccc acgtggttgc agataacctc 1650  
 gacctggtgc cttaggtgtg gctgagccca ctctcccgag ggcgcctcca 1700  
 agggggggcc acttgaaaag tgaataaatg gggcggtttc ggaagcgtca 1750  
 ggttttccat gttatggtc tctctgcgtt tgaataaaga ctatctctgt 1800  
 tgcctacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys  
 1 5 10 15  
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly  
 20 25 30  
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile  
 35 40 45  
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr  
 50 55 60  
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala  
 65 70 75  
 Ala His Ser Ser Arg Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val  
 80 85 90  
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala  
 95 100 105  
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val  
 110 115 120  
 His Glu Val Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln  
 125 130 135  
 Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His Ser Leu Val Ser  
 140 145 150  
 Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe Val Gly Val  
 155 160 165

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala	171	175	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe	185	190	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val	200	205	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	215	220	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr	230	235	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala	245	250	255
Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser	260	265	270
Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser	275	280	285
Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser	290	295	300
Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro	305	310	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys	320	325	330

Val

<210> 237  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Synthetic oligonucleotide probe

<400> 227  
 -caggaatgac aggggaagag gg 22

<210> 238  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Synthetic oligonucleotide probe

<400> 238  
 -caggactcgc tacgtcgc 18

<210> 239  
<211> 14  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
cagcccttc tctccttcc tccc 24

<210> 240  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 240  
ccagtatca gggargcact cagcc 25

<210> 241  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 241  
ccagccagag gcagatag 18

<210> 242  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 242  
cggtcacccgt gtctcgoggg atg 23

<210> 243  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
cagcccttc tctccttcc tcccacgtcc tatctgctc tc 42

<210> 244

<211> 1894  
<212> DNA  
<213> Homo sapiens

<400> 244  
gggggggtcc gtgaggggggt cctttgggga ggggtagtgt ttggtgtccc 50  
tgtcttgogt gatattgaca aactgaagct ttctgcacc actggactta 100  
aggaagagtg taactgtagg cggacagctt tagtggcggg ccggccgctc 150  
tcaccccccg taaggagcag agtcttttgt actgaccaag atgagcaaca 200  
ctacatcca ggagctccc accaatggga aggttttatt gaaaactaca 250  
gtgggagata ttgacataga gttgtgggtc aaagaagctc cttaaagcttg 300  
cagaaatttt atcaactctt gtttggaaag ttattatgac aataccatct 350  
ctcatagagt tgtgcttggt ttcatagtcc aaggcggaga tcttactggc 400  
acagggagtg gtggagagtc tatctatgga ggcgcattca aagatgaatt 450  
tcattcacgg ttgcttttta atcggagagg actggctgcc atggcaaatg 500  
ctggtctctc cgataatggc agccagtttt tcttcacact gggtcgagca 550  
gatgaactta accaataagca taccatcttt ggaaagggtta caggggatac 600  
agtatataac atgttgogac tgtcagaagt agacattgat gatgacgaaa 650  
gaccacataa tccacacaaa ataaaaagct gtgaggtttt gtttaatcct 700  
tttgatgaca tcattccaag ggaaattaaa aggttgaaaa aagagaaaac 750  
agaggaggaa gtaagaaat tgaacccaa aggcacaaaa aattttagtt 800  
tacttcactc tggagaggaa gctgagggaag aagaggagga agtaaatcga 850  
gttagtcaga gcctgaaggg caaaagcaaa agtagtcctg acttgcttaa 900  
ggatgatcca catctcagtt ctgttcacgt tctagaaagt gaaaaaggtg 950  
atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000  
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgcaca 1050  
aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100  
aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150  
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200  
tgcajcaaaa caagcagaaa aaagaagtga agaggaagaa gccctccag 1250  
atggtgctgt tgccgaatac agaagagaaa agcaaaaagta tgaagctttg 1300

aggaagcaac agtcaagaa gggaacttc cggaagata agacccttgc 135  
 actjctgaac cagtttaaat ctaaactcac tcaagcaatt gctgaaacac 140  
 ctgaaaatga cacttcctgaa acagaagtag aagatgatga aggatggatg 145  
 tcaatgttac ttcagtttga ggataaaaag agaaaagtga aagatgcaag 150  
 catgcaagac tcagatacat ctgaaatcta tgatctcgg aatccagtga 155  
 ataaaagaag gaggggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 160  
 agaagataaa atgagaataa cgataaccag aacttgctgg aaatgtgoot 165  
 acaatggoot tgaacagcc attgttcaca acagcatcac ttaggggtgt 170  
 gaaaagaagt atttttgaac ctgttgcttg gttttgaaaa acaattatct 175  
 tgttttgcaa attgtggaat gatgtaagca aatgcctttg gtaactggtg 180  
 catgtgttcc ttcctagtctg accctttata ttgctaaatc tgaataaaaa 185  
 taactttcct tcacacaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245  
 <211> 472  
 <212> PRT  
 <213> Homo sapiens

<400> 245  
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val  
 1 5 10 15  
 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser  
 20 25 30  
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu  
 35 40 45  
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly  
 50 55 60  
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly  
 65 70 75  
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg  
 80 85 90  
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly  
 95 100 105  
 Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala  
 110 115 120  
 Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly  
 125 130 135



Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp  
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg  
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met  
455 460 465

Arg Glu Lys Lys Gln Arg Arg  
470

<217> 246  
<218> 24  
<219> DNA  
<220> Artificial Sequence

<221>  
<222> Synthetic oligonucleotide probe

<223> 245  
ctaggagatc ctactggcac aggg 24

<224> 14  
<225> 18  
<226> DNA  
<227> Artificial Sequence

<228>  
<229> Synthetic oligonucleotide probe

<230> 14  
ctagtttagtc agagcatg 18

<231> 248  
<232> 18  
<233> DNA  
<234> Artificial Sequence

<235>  
<236> Synthetic oligonucleotide probe

<237> 248  
cagatgggagc tggtagcg 18

<238> 249  
<239> 24  
<240> DNA  
<241> Artificial Sequence

<242>  
<243> Synthetic oligonucleotide probe

<244> 149  
caactggcac aggaactgag atgtggatc 29

<245> 250

<111> 24  
<111> DNA  
<111> Artificial Sequence

<120>  
<120> Synthetic oligonucleotide probe

<400> 250  
ctgggttcagc agtgcaaggg tctg 24

<110> 251  
<111> 15  
<111> DNA  
<111> Artificial Sequence

<120>  
<120> Synthetic oligonucleotide probe

<400> 251  
ccctctccgat taaaaagg 18

<110> 252  
<111> 45  
<111> DNA  
<111> Artificial Sequence

<120>  
<120> Synthetic oligonucleotide probe

<400> 252  
gagagagctg gttgcacatgg caaatgctgg ttctcatgat aatgg 45

<110> 253  
<111> 1456  
<111> DNA  
<111> Homo sapiens

<400> 253  
gggggggggtt ggggctggaa gttcccgcca ggtccgtgac gggcgagaga 50  
gagagcgccc ggcccgccctt ggctttgagg cgagagaagt gtcccagacc 100  
catcttcgctt tgcctgacggc gtccagccctt ggccagacat gtccacaggg 150  
ttctctcttg ggtccgggac tctggggctcc accacgttgg ccgcgggggg 200  
gacacagaca gggggggttt tctccttcgg aacgggaacg tctagcaacc 250  
cttctctgggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300  
actacatctg ctccctcaag tggttttgga accgggctct ttggatctaa 350  
aactgcaact gggttcaact taggaggaac aaatacaggt gccttgcaca 400  
ccagagagcc tcaagtggtc accaaatatg gaacctgca aggaaaaacag 450  
atgcctgttg ggaagacacc catccaagtc tttttaggag tccccttctc 500

cagacotcct ctaggatatcc tcagggtttgc acctccagaa cccccggagc 550  
cctggaaagg aatcagagat gtaaccaact acccgccctgg atggagtctc 600  
gtctctgtgc caggctggag tgcagtgga ccatctcggc tcaactgcaac 650  
ctccgcctcc cgggttcaag cgagctcctc gctcagcct ctgagtgctc 700  
ggggtacacg gtgcctgcag gagtccctggg gccagctggc ctcgatgtac 750  
gtcagcacgc gggaacggta caagtggctg cgttccagcg aggaactgtc 800  
gtacctgaac gtgtacgggc cggcgcgcggc gcccggggat ccccaagctg 850  
cagtgatggt ctgggtcccg ggaggcgccct tcatcgtggg cgttgcttct 900  
tcgtacgagg gctctgaact ggccgcgcgc gagaaagtgg tgcgtggtgt 950  
ctcgagcac aggtctggca tcttcggctt cctgagcacg gacgacagcc 1000  
accgcgcggg gaactggggg ctgctggacc agatggcggc tctgggctgg 1050  
gtgcaggaga acatcgacgc ctcgggggga gaccaggaa atgtgacct 1100  
gttcggcacg tcggcggggg ccacgagcat ctcaggactg atgatgtcac 1150  
ccctagccctc gggctctctc catcggggca tttcccagag tggcacgcgc 1200  
ttattcagac ttttcacac tagtaaccca ctgaaagtgg ccaagaaggt 1250  
tgcccaactg gctggatgca accacaacag cacacagatc ctggtaaac 1300  
gctcgagggc acctacaggg accaagggtg tgcgtgtgtc caacaagatg 1350  
agattcctcc aactgaact ccagagagac ccggaagaga ctatctggtc 1400  
catgagccct gtgggtggat gtgtgggtgat ccagatgac cctttgggtc 1450  
tctgaacca ggggaaggct tcatctgtgc cctaccttct aggtgtcaac 1500  
aacctggaat tcaattggct cttgccttat aatatcaca aggagcaggt 1550  
accacttggt gtggaggagt acctggacaa tgtcaatgag catgactgga 1600  
agatgctacg aaaccgctat atggacatag ttaagatgc cacttcgtg 1650  
tatgcacac tgcagactgc tcactaccac cgagaaaccc caatgatggg 1700  
aatctgcctc gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750  
ggattttacc acaagagtgg gcatgaagct caaggagaag aagatggctt 1800  
tttggatgag tctgtaccag tctcaaagac ctgagaagca gagycaattc 1850  
taaggggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1900

caggccctgg ggagactago catggacata cctggggaca agagttctac 1950  
 ccaacccagt ttagaactgc aggagctccc tgcctgctcc aggcocaaagc 2000  
 tagagctttt gctgtgtgtg tgggaactgc actgaccttt ccagcctgac 2050  
 atcccatgat gccctctac ttcactgttg acatccagtt aggcacagga 2100  
 ctgtcaaacac cacactgtgc ccagctctcc agcctcagga caacctcttt 2150  
 tttcccttc ttcacatcc ccacaccttc aatgtctct tgtgactct 2200  
 tottatggga ggtcgaccca gactgcact gccctgtcca ctgcacccag 2250  
 cctggcattt accatccatc ctgtcaaac ttgttcctgt ctgtccat 2300  
 tggcctggag gactaggga ggtgtgtgaca tggagcaaac ccttggtagt 2350  
 tgggatctt ctctccacc cacacttata tcccccaggg ccactccaaa 2400  
 ctctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450  
 aaaaaa 2456

<110> 254  
 <111> 545  
 <112> PFT  
 <113> Homo sapiens

<400> 254  
 Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr  
 1 5 10 15  
 Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe  
 20 25 30  
 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly  
 35 40 45  
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser  
 50 55 60  
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly  
 65 70 75  
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg  
 80 85 90  
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met  
 95 100 105  
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe  
 110 115 120  
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro  
 125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Gln	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Gln	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro  
425 430 435

Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu  
440 445 450

Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn  
455 460 465

Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp  
470 475 480

Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met  
485 490 495

Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr  
500 505 510

Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala  
515 520 525

Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu  
530 535 540

Pro Gln Glu Trp Ala  
545

4010- 255

4011- 25

4012- DNA

4013- Artificial Sequence

4020-

4021- Synthetic oligonucleotide probe

4400- 255

aggagcctgc aggaactctg ggg 23

4010- 256

4011- 24

4012- DNA

4013- Artificial Sequence

4020-

4021- Synthetic oligonucleotide probe

4400- 256

ccacccagg aagccgaaga tgcc 24

4010- 257

4011- 25

4012- DNA

4013- Artificial Sequence

4020-

4021- Synthetic oligonucleotide probe

<400> 257

gaaggtatca agtgggtgag ctccagcag gactgtctgt acctg 45

<210> 159

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 158

gagaaagggc ctgtctcagg caggccctgc gctcctatg cggagatgct 50

actgcacatg ctgtctgctc cgtctgtggg cgggtcccag gctatgggatg 100

ggaattctg gatacagatg caggagtcag tgatggtgac ggagggcctg 150

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00100 259

00110 544

00120 PRT

00130 Homo sapiens

04000 259

Met	Leu	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Gly	Gly	Ser	Gln
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Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
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Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
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Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75

Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
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Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105

Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
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Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
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Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
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Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
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Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
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Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210

Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

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caacagaaaa ctctcaaaaca aagaaagtca agcagccagt gcgatctcat 150  
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 <212> PRT  
 <213> Homo sapiens  
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				20					25					30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	
				35					40					45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	
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His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Gln	Phe	Val	
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Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Gln	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Gln	Gly	Thr	
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Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
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Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
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Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
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Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
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Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
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Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser	
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Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile	
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Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Iyr	
				320					325					330	
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu	
				335					340					345	
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln	
				350					355					360	
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr	
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Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly	
				380					385					390	
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg	
				395					400					405	
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly	
				410					415					420	
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Tyr	
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Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln	
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Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp	
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His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu	
				470					475					480	
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp	
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Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser	
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Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln	
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Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu	
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Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn	
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Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val	
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Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	
				575					581					585	
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	
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Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	
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Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	
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Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	
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Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	
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Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	
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Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Ser	
				695					701					705	
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	
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Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	
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Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	
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Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	
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aagaaattt ataccgcttg actgtntgt aatctgcacc cactgggant 250  
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ccgcgcttaa cttctcgcg ggggcgcagc caccttcggg agtccggggt 150

gcccacctgc aaactctccg ccttctgcac ctgcacccc tgagccagcg 230  
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 cattctcgcc ttctgggat ggatcggygc catcgccagc actgcctgc 300  
 cccagtggag gatttactcc tatgcggggg acaacatcgt gacggcccag 350  
 gccatgtacg aggggctgtg gatgtcctgc gtgtcgacg gcacggggga 400  
 gatccagtgc aaagtctttg actccttcgt gaatctgagc agcacattgc 450  
 aagcaacccg tgccttgatg gtgggtggga cctcctggg agtgatagca 500  
 atcttttggg ccaccgctgg catgaagtgt atgaagtgt tgggaagcga 550  
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 gttcaagaat cctatgaccc tatgacccc gtcaatgcac ggtacgaatt 700  
 tggtcaggct ccttctactg gtcgggtgc tgcctctctc tgcctctgg 750  
 gaggtgcctt actctgctgt cctgtccccc gaaaaacaa cctttaccca 800  
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 gtgacacaga ggcaaaaagga gaaaatcatg ttgaaaacaa ccgaaaatgg 900  
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 aatctgaagt atggtattac aaaaacaaac aacaaacaaa aaacccatgt 1000  
 gttaaaaata cagtgctaa acatggctta atcttatttc atcttctctc 1050  
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 gtaatcatac tcaaatgggg gaaggggtgc ccttaataa tatatagata 1150  
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 caagctaccc ccatgtgatt cactgccttc ctctctctac cagtctattt 2200  
 ccaactgaaca aaacctacac acataccttc atgttggtta gtgccttccc 2250  
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 gatgtgttgg ggatccagtg agatagaata catgtaagtg tggttttgta 2650  
 atttaaaaaag tgcctatact agggaaaajaa ttgaggaatt aactgcatac 2700  
 gtttcgggtg tgccttttcaa atgtctgaaa ataaaaaaaaa tgtttaag 2747

<210> 270  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 270  
 Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe  
 1 5 10 15  
 Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

	20	25	30
Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala	35	40	45
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly	50	55	60
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser	65	70	75
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu	80	85	90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met	95	100	105
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val	110	115	120
Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val	125	130	135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Gln Phe Tyr Asp	140	145	150
Pro Met Thr Pro Val Asn Ala Arg Tyr Gln Phe Gly Gln Ala Leu	155	160	165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala	170	175	180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr	185	190	195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr	200	205	210

Val

<111> 171  
 <111> 164  
 <111> DNA  
 <111> Homo sapiens

<111>  
 <111> unsure  
 <111> 1, 63, 163, 434, 436, 444  
 <111> unknown base

<400> 171  
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 ctccctatgc tggcgacac atcgtgaccg ccagaccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgtgaato tgagcagcac attgcaagca acccgtgpcr 250  
 ctatgggtgt ttggcaccctc ctgggagtgga tagcaatctt tctgggcacc 300  
 gttggcatga agtgatatgaa gtgcttggaa gacgatgagg tgcagaagat 350  
 gaggatggct gtcattgggg ggcgatatt tctcttgcg ggtctggcta 400  
 ttttagctgc cacagcatgg tatggcaata gaancttca acantctat 450  
 gacccatga cccagtcac tgcaggtao gaatttggc aggcctctct 500  
 ccctggctgg gctgctgctt ctctctgctt tctgggaggt ggcctacttt 550  
 gctgtcctg tccc 564

<210> 272  
 <211> 498  
 <212> DNA  
 <213> Homo sapiens

<210>  
 <211> unsure  
 <212> 30, 49, 102, 141, 147, 171, 324-325, 339-341  
 <213> unknown base

<400> 272  
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 tccagatgtt gggcttcatt ctccctctcc tgggatggac cggcgcccat 100  
 cttcagcact ggcctgcccc agtggaggat ttactcctat nccggcnaca 150  
 acatctgac cgcacaggcc ntgtacgagg ggcctgtgat gtcctggctg 200  
 tgcagagaca cggggcagat ccagtgcaaa gtctttgact cccttgctga 250  
 atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcacc 300  
 ctcttgag tgatagcaat cttnntggcc accgttgtnn ntgaagtgtg 350  
 tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggcctgcatt 400  
 cggggggaga tattctctct tgcaggtctg gctattctag ttgcacagc 450  
 atgttatgc aatagaatcg ttcaagaatt ctatgacct atgacaga 498

<210> 272  
 <211> 552  
 <212> DNA  
 <213> Homo sapiens

<210>  
 <211> unsure

4232> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
4233> unknown base

4410> 173

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gatgaanaga gccatctctca gactccctgc cccatggaga ttttncctat 100  
ctcggcgaca acatcttgac ccccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccc ggcagatcca gtgcacagtc tttgactcct 200  
tcttgactct gngcagcaca ttgcagcaac ccctggccctg atgggtgggtg 250  
ccatccctcc gggagtgata gcaatctttg tggccacccg tggcatgaag 300  
tgtctgaagt gotttggaaga ccatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcatatcttc ctcttgccag tctggctatc tnnngctggc 400  
acaccatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450  
cccagtcacat gccaggtacg aatttggtca ggcctcttc actggctggg 500  
ctgtgtcttc ctctgctctt cggggaggcg ccttactttg ctgtccctgc 550  
ga 600

4410> 174

4411> 326

4412> DNA

4413> Homo sapiens

4421>

4421> unsure

4422> 13, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 406-407

4423> unknown base

4430> 174

attctccctc cctggatgga tagcnccacc gtcacattgc cttcccccan 10  
tggcggaatn actcctatgc ttggcgacac atcgtgaccc cccaggccat 100  
ctacccaggg gctttggatg tcttgctgtg ccagagccac cgggcagatc 150  
ccagtgcaca gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
caaaccgtgc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
ttgtgccac cgttggcatg aagtgtatga agtgcttggc agacgatgag 300  
gtgcacagaag atgaggatgg ctgtccattg gggcgcgata tctcttgttg 350  
caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400  
cnnngnntct atgacctat gaccccagtc aatgccaggt acgaatttgg 450

tcaaggtctctc ttcaactgggtc ggggtgctgc ttctctctgc cttctggggag 500

atgacctact ttgctgttcc tgcacc 526

<111> 275  
<111> 293  
<112> DNA  
<113> Homo sapiens

<118>  
<111> unsure  
<112> 21, 61, 91, 144, 233-239, 262, 265-266, 271, 274  
<113> unknown base

<119> 275  
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gacacacatt ncaagcaacc ccttgcccttg aaggctgggtg acatccccc 100  
tggaaatgaa tagcaatcctt cgtgggcaccc gttgggcacga agtctatgaa 150  
ngctctgaa gacgatgagg cgcagaagat gaggatggct gtcattgggg 200  
ggagatcatt tcttctctgca ggtctggcta ttttagtctc cacagcatgg 250  
tatggcata gnatctctcg nggtctctat gacccatga cccagtcac 300  
tgcaggtac gaatttggtc aggtctctct cactggctgg gctgctgctt 350  
ctctctgctt cctgggaggt gccctacttc gctgttcttg tcccogaa 395

<120> 276  
<121> 435  
<122> DNA  
<123> Homo sapiens

<124>  
<121> unsure  
<122> 29, 58, 130, 234, 314, 364, 427, 450, 461, 476  
<123> unknown base

<125> 276  
agcaatgcac tgcacccagt ggaggattaa ttctatgnt ggggacacaa 50  
ttgtgaonco ccaggccatg taaggggggc tgtggatgtc ctgctgtctc 100  
cagagcaacg ggcagatcca gtgcacagtn ttgactcct tgcctgaattt 150  
gagcagcaca ttgcaagcaa cccgtgcctt gatggctggtt ggcattcttc 200  
tcgagtgat agcaatcttt gtgggcaccc tggnaatgaa gtgtatgaag 250  
tccttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300  
cgcctatattt cctnttgcag gtctggctat tttagttgac acagcatggt 350  
atgycaatag aatngttcaa gaattttatg accctatgac cccagtcac 400



gcagaggtacg aatttggtea ggcttnttcc actgggtggg ctgctgcttn 450

ttctgcttc ntgggaggtg cctantttg ctgttctgc gaacc 495

<110> 277  
<111> 200  
<112> DNA  
<113> Homo sapiens

<120>  
<121> unsure  
<122> 34, 37, 133, 147, 163, 165-166, 172  
<123> unknown base

<130> 277  
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cacagcatgg tatggcaata gaatcttca agaattntat gacctatga 100  
cttcagtcac tgcaggtac gaattgggc aggtctntc cactggntgg 150  
ctgtctgctt ctntnngct tntgggaggt gcctacttc gctgtctcg 200

<110> 14  
<111> 842  
<112> DNA  
<113> Homo sapiens

<120>  
<121> unsure  
<122> 16, 43, 55, 77, 193, 361-362, 391-392, 396  
<123> unknown base

<130> 278  
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gggtctgga atgcccggc tgcaccagag caccgggcag atccagtgc 150  
tajctcttga ctcttctgtg aatctgagca gcacattgc agcaacctg 200  
cttctgctgt ggttggcctc ctcttgggag tgatagcaat ctttctggc 250  
acctctggca tgaagtgtg tgaagtgtt ggaagacat gaggtgcaga 300  
agatgaggat ggtctcatt gggggcgoga tttctctct tgcaggtctg 350  
gctatcttag nngccacaga atggtatggc aatcagaccc nntcnaaac 400  
tctatgcacc tatgacccca gtcaatgcca ggtacgaatt tggtcaggct 450  
ctcttcactg gctgggctgc tcttctctc tgccttctgg gaggtgcct 500  
actttgtgt tctgtcccc gaaaaacaac ctcttaccca cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 115, 147, 228, 327  
<223> unknown base

<240> 279  
gggggtgca gctgttgggc ttcattctgc ttctgtggat ggaatcggcg 50  
ccatcttcag cactgcccctg ccccatggag gatttactcn tatgctggcg 100  
acacactcgt gacccccag gccatgtacg aggggctgtg gatgtcngcg 150  
ctctgtagag caccgggcag atccagtgcg aagtctttga ctctctgctg 200  
aatcttagca gcacattgca agcaacctg ccttgatggt ggttggcctc 250  
atcttgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtctctg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350  
ggggcctgat atttctctct gcaggtctgg ctattcttag ttgcacacag 400  
atggtctggc aatagaatcg ttcaagaatt ctatgacct atgaccccag 450  
tcaatgcag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500  
ctttctctct gcttctggg aggtgcctca cttgtctgtt cctgcgaa 548

<210> 210  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<240> 210  
ccacccagtc atggccaaag c 21

<210> 251  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<240> 251  
gttccacag tagtctttcc cgtcgg 26

<210> 242  
<211> 43

4012 - DNA  
4013 - Artificial Sequence

4020 -  
4021 - Synthetic oligonucleotide probe

4401 - chr2  
ctgcagctgt tgggttcac tctgccttc ctgggatgga tgc 43

4011 - chr3  
4011 - chr5  
4012 - DNA  
4013 - Homo sapiens

4401 - chr3  
gggtggagtc agctggccgg gacccggggc ctggccctcg cctccggccc 50  
ctggcctgc accggctaga ccgacccccc cctccagcgc gccacccggg 100  
tagaggaccc ccggccgtgc ccggacgggt cccggccttt ttgtaaaaact 150  
taaagcgggc gcagcattaa cgtctccgcg ccgggtgacc tctcaggggt 200  
ctcccccaca aagggtgctcc gccgctaagg aacatggcga aggtggagca 250  
ggtctcagc ccggagccgc agcacgagct caaattccga ggtccctcca 300  
ccgctgttgt caccaccaac cttaaagctg gcaaccgac agaccgaat 350  
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caatagcgga atcatcgatg cagggggccc aattaatgta tctgtgatgt 450  
tacagccttt cgattatgat cccaatgaga aaagtaaaaca caagtttatg 500  
cttcagttta tgtttgctcc aactgacact ccagatatgg aagcagtatg 550  
gaaggatgca aaaccggaag accttatgga ttcaaaaact agatgtgtgt 600  
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attatatcca caactgcctc aaagacagaa acaccaatag tgtctaagtc 700  
ctcgagttct cctttggatg acacccaagt taagaaggct atggaagaat 750  
gtaagatgct gcaaggcgaa gttcagaggc taaggagga gaacaaggcag 800  
ttcaaggaaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccattcca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
ggctcttggc tctggtggtt ttgtcttcta cgttgggtgt aattattggg 950  
aagattgctt tctagaggta gcatgcacag gatggtaaat tggattggtg 1000  
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaaga 1050

aattaatgta tgatgacata tcacaaggtct tgcctttaaa ttacccctcc 1170  
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1180  
ttagaaagt ttaaaatgtat agtaactgat tgagggggaa aaagaatgat 1210  
ctttattaat gacaagggaa accatgagta atgcacacat ggcattattg 1220  
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ctcttaaaa tgacacccct cctcgccctg tgggtgctggc cctgggggag 1260  
ctggagccca gcatgctggg gagtggggc agtccacac agtagtccc 1290  
acgtggccca ctccggccc aggtgcttt cctgtcttc agttctgtcc 1320  
aagccatcag ctccctggga ctgatgaaca gactcagaag cccaaaggaa 1330  
ctgcaactgt gacgacccag acgtactgt cataagttag aggtgtgtgt 1350  
tgactgattg accagcgtct ttggaaataa atggcagtgc ttgttcact 1360  
taaggggacc aagctaaatt tctattggtt catgtagtga agtcaaatg 1370  
ctattcagag atgtccaatg catatttaac ttatttaatg tatttcact 1380  
catgtttctt tattgtcaca agagtacagt taatgctggg tctgtctgaa 1390  
ctctgttggg tgaactggta ttgtgtgtg agggctgtgg gctctctgt 1400  
ctctggagag ctctggcatg tggaggtggg gttatttggg atgtggaga 1410  
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ccacccaatc ctctcagtag tagttgagag ttgactgtg aattaatttt 1480  
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agaaaatta taataaagcc ccaaaattaa gaaaa 1500

<210> 234  
<211> 243  
<212> PRT  
<213> Homo sapiens

<400> 234  
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Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu	20	25	31
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	61
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	91
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	101	106
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val	125	131	136
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	161	166
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	181
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	211
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys	230	235	240
Ile Ala Leu			

<110> 235  
 <111> 418  
 <120> DNA  
 <130> Homo sapiens

<200>  
 <210> unsure

<222> 40, 53, 63, 119, 134, 177-178, 255  
<223> unknown base

<400> 285  
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ctcccajtcag gacaatggnt cgggctgcag aggnntagaa ggcaggggcac 150  
cagracctctt gggctggggag caagggngga gagaaaactct ccagcgaatc 200  
ctcttagctac tagctgagag ttgactgtg aattaattct atgcacataaa 250  
ajcncacccc agtctctgtct gactatgtag catcttgaaa agaaaaatta 300  
caataaagcc ccaaaaattaa gaattctctt gtcattttgt cacattctgt 350  
ctatgggggg aattattact tcatcattct tattattctg ccattgggaag 400  
gttcacctta aaatgagc 418

<224> 286  
<225> 283  
<226> DNA  
<227> Homo sapiens

<228>  
<229> unsure  
<230> 83, 97  
<231> unknown base

<400> 286  
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gattacctcc ttaaatgaca ccttctctg cctgttggg ctggcccttg 100  
cgtacgttga gccccagcat gctggggagt ggggtcagct ccacacagta 150  
gttcccacgt ggcccactcc cggcccagga tgcttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggaactga tgaacagagt cagaagccca 250  
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caactcttat ccagagatgt ttaatgcata ttttaactat ttaattgatt 450  
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<210> 287  
<211> 270

<212> DNA  
<213> Homo sapiens

<221>  
<221> unsure  
<222> 31, 64, 72, 164, 198, 200, 220, 222, 229, 242  
<223> unknown base

<400> 247  
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tatatctatg ggatttaaat ttatcataac catgtgtaaa aagaaattaa 150  
tctatctga catntccacg gtattgcctt taaattaccc atccctgnan 200  
atccatccac agatcacacn anacaaatnt aatgtaacga ttttttagaa 250  
atttataaat gtatagtaac 270

<212> DNA  
<213> Homo sapiens

<221>  
<221> unsure  
<222> 31, 116, 129, 197, 273, 294, 297, 349, 351  
<223> unknown base

<400> 348  
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gcactygggc agcatnagac gtacttgtna taagtgcagag gogtctgttg 150  
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aagggtccaa gctaaatttg tattgggttca tgtagtgaag tcaaaactgtt 250  
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tattttctta ttgtccaaag agtacagtta atgctgcgtg ctgctgaant 350  
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ttccatgctt tggctatgtg gaggtggg 423

<212> DNA  
<213> Homo sapiens

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gaaataaatg gcagtgtttt gttcacttaa agggaccaag ctaaatttgt 200  
attgggttcat gtagtgaagt caaactgtta ttacagagatg tttaatgcat 250  
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gtacagttaa tgcgtggtgc 320

<310> 290

<311> 609

<312> DNA

<313> Homo sapiens

<320>

<331> unsure

<332> 57, 60, 136, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 431, 513, 532, 534, 598

<333> unknown base

<400> 290

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cttcctagac tcttgggtgc ggccttggg gagctngagc ccagcatgct 200  
gggagtgag gtctgtcca cacagtatgc ccangtggc ccantccgg 250  
ccaggttgc ttccgtgtc ttacgttctg tccaagccat cagctccttg 300  
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ctattgtctg 609

<410> 291

<411> 493

<412> DNA

<413> Homo sapiens

<420> 291



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<211> 100  
 <211> 27  
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<22>  
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<211> 103  
 <211> 13  
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<22>  
 <223> Synthetic oligonucleotide probe

<400> 100  
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<211> 104  
 <211> 50  
 <211> DNA  
 <211> Artificial Sequence

<22>  
 <223> Synthetic oligonucleotide probe

<400> 104  
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<211> 106  
 <211> 1360  
 <211> DNA  
 <213> Homo sapiens

<400> 295

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gctctgatct cagctgacag tgcctcggg gacaaacaa gctgggcagg 150  
gtctcacttt gttgcccagg ctggagttca gtgcacgat catgggttac 200  
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(210) 296  
 (211) 413  
 (212) PRT  
 (213) Homo sapiens

(400) 296  
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 1 5 10 15  
 Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

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				35					40					45
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr
				50					55					60
Val	Cys	Gly	Ile	Gln	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu
				65					70					75
Ser	Gln	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Gln	Thr	Val	Phe	Glu	Asn
				80					85					90
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu
				95					100					105
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg
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Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp
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Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu
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Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu
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Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly
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Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser
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Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala
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Ser	Gly	Gly	Asp	Gln	Arg	Glu	Gly	Thr	Arg	Glu	His	Leu	Gln	Glu
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Arg	Ala	Lys	Gly	Gly	Arg	Arg	Arg	Lys	Lys	Ser	Gly	Arg	Gly	Gln
				230					235					240
Arg	Ile	Ala	Glu	Gly	Arg	Pro	Ser	Phe	Gln	Trp	Thr	Arg	Val	Lys
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Asn	Thr	His	Ile	Pro	Lys	Gly	Trp	Ala	Arg	Gly	Gly	Met	Gly	Asp
				260					265					270
Ala	Thr	Leu	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Arg	Ala
				275					280					285
His	Lys	Lys	Lys	Tyr	Met	Glu	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Lys
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Lys	Met	Pro	Gly	Gly	Met	Ile	His	Phe	Ser	Gly	Phe	Asp	Asn	Asp

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp Glu	
330	335	336
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly Ser	
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys Lys	
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val	Tyr Ser Gly His Gln Trp	
365	370	375
Val Asp Val His Gly Val Gln Lys Asp	Tyr Asn Val Ala Val Arg	
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His Gly	
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 197

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

gcacatctgcag gagagagccg aggg 24

<210> 198

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ccatcgtccccc gtgaatccag aggc 24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

gaagggaggg cttcctttca gtggaccgg gtcaagaata ccac 45

<210> 200

4211 1869

4212 DNA

4213 Homo sapiens

4400 300

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 caagtgaat catctacca aagctttttg gctctcaaat caagattga 1850  
 ctactttca aaaaaaaaa 1869

0010: 301  
 0011: 525  
 0012: PET  
 0013: Homo sapiens

0000: 311  
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 20 25 30  
 Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys  
 35 40 45  
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
 50 55 60  
 Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr  
 65 70 75  
 Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala  
 80 85 90  
 Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe  
 95 100 105  
 Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser  
 110 115 120  
 Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala  
 125 130 135

Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp	
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				170					175					181	
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln	
				185					190					191	
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr	
				200					205					210	
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu	
				215					220					225	
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Gln	Asn	Ser	
				230					235					240	
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp	
				245					250					255	
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro	
				260					265					270	
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala	
				275					280					285	
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg	
				290					295					300	
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly	
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Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn	
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Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile	
				335					340					345	
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro	
				350					355					360	
Ala	Ser	Asp	Gly	Tyr	Lys	Gln	Ile	Met	Pro	Tyr	Asp	Leu	Tyr	His	
				365					370					375	
Pro	Leu	Pro	Arg	Trp	Glu	Ala	Thr	Pro	Trp	Thr	Ala	Cys	Ser	Ser	
				380					385					390	
Ser	Cys	Gly	Gly	Gly	Ile	Gln	Ser	Arg	Ala	Val	Ser	Cys	Val	Glu	
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Glu	Asp	Ile	Gln	Gly	His	Val	Thr	Ser	Val	Glu	Glu	Trp	Lys	Cys	
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Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

0210 - 502  
 0211 - 1533  
 0212 - DNA  
 0213 - Homo sapiens

0400 - 502  
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 ccagggggtg cgcagagggt ggggacgggg cctcatggac ggggaagactg 200  
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 gagctgggac tgggctgggt gggctgggtt cgggctttct ggcaggaaaat 450  
 gcttcaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500  
 tccagtggcc tcatatgaag actgaagatg ggtttgagat gcagttcggg 550  
 gtgaaccatc tgggggactt ctactcacc aatcttctcc ttggactctt 600  
 caaagctca gctcccgaca ggattgtgtt agttttctcc aaactttata 650  
 aatcgggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
 aaaagctttt gttatagcgg gagcaaaactg gctaaccatc tttttaaccag 750

ggaactagcc ggccgcttag aaggcacaaa tgcacccgtc aatgtgttgc 800  
 atcttggtat tgcacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcbaa ttctgtgtca tgggtttttt ccaaaactcc 900  
 agtagaaggt gccacagactt ccatttattt ggctcttca cctgaggtag 950  
 aaggagtgtc aggaagatac ttctgggaatt gtaaaagagga agaactgttg 1000  
 cccaaagcta tggatgaato tcttgcaaga aaactctggg atatcagtga 1050  
 agtjatggtt ggctgtctaa aataggaaca aggagttaaa gagctgttta 1100  
 taanaactga tctcagttat atctgtgato aggaatgggt tggattgaga 1150  
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtattttgg agttactgaa aaattatttc tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tcttaagtat aatgaataat 1300  
 aagtcacatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350  
 tggatgacat attaatattt gtcagaatta agtgactcaa agtctatctg 1400  
 agaggttttt caagtatctt tgagtctcat ggcbaaagtg ttaactagtt 1450  
 ttactacaat gtttgggtgt tctgtggaaa tctctgctt ggtgtgtgca 1500  
 cacaagctctt acttggcata aatttactgg tac 1533

(210) 303  
 (211) 316  
 (212) PRT  
 (213) Homo sapiens

(400) 303  
 Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly  
 1 5 10 15  
 Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln  
 20 25 30  
 Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr  
 35 40 45  
 Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly Arg Ala Thr Ala  
 50 55 60  
 Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met Gly Cys Arg  
 65 70 75  
 Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg Arg Glu  
 80 85 90  
 Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser Gly

95					100					105				
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg
				110					115					120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg
				125					130					135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr
				140					145					150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His
				155					160					165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys
				170					175					180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr
				185					190					195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser
				200					205					210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile
				215					220					225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Gln	Gly	Thr	Asn	Val
				230					235					240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly
				245					250					255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu
				260					265					270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr
				275					280					285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly
				290					295					300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala
				305					310					315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val
				320					325					330
Met	Val	Gly	Leu	Leu	Lys									
				335										

<110> 3/4  
 <110> 5/1  
 <120> DNA  
 <130> Homo sapiens

<200>  
 <220> unsure

<222> 31, 34, 62, 87, 221, 229

<223> unknown base

<400> 204

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gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100  
gganccaggga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
tttcatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250  
actgaanaat ctttttggg ataagagaat ttacgcaaag atgttttaaa 300  
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
atttttaaat tataactggg caagcacgga tgacatatta atatttgcca 400  
aaattagtgt actcaaatgt ctatcgagag gtttttcaag tatctttgag 450  
tttcattgac aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
tggaaattat ctgcctggct t 521

<210> 305

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccacgaaatg ctccaggaag agcc 24

<210> 306

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

cccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aaagcaggga ttttccagtg ccttccatg aagactgaag atggg 45

1210 + 308  
1211 + 1523  
1212 + DNA  
1213 + Homo sapiens

1400 + 318  
gagaggagga ggtggcgctg cctggagaat cctccgctgc cgtcggctcc 50  
aggagcccag ccccttccca acccaaccca acctagccca gtcccagccg 100  
ccagcgccctg tccctgtcac ggaccccagc gttaccatgc atcctgcctg 150  
cttccctatcc ttacccgacc ccagatgctc ccttctgctc ctggtaacct 200  
gggtttttac cccctgaaca actgaataa caagtcttgc cacagagaat 250  
atagatgaaa ttttaacaaa tctgtatgtt gctttagtaa atttttatgc 300  
tgaatgggtg cgtttccagtc agatgttgca tccaattttt gaggaagctt 350  
ccgatgtcat taagggaaga tttcccaatg aaaatccagt agtgtcttgc 400  
agatctgatt gtgaccagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500  
aatccagggg ccagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccc 600  
ctctgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650  
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaacgg aaagatatag 750  
tggcgacaa acatcttaca aaccaccagg gcattctgtt ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
gataaatgtg ttcctctgtt ccgagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc ctttctcat actctttcac atgaaagaag 950  
atacagaaag tttagaaata ttcagaaatg aagttagctg gcaattaata 1000  
agtgaaaaaag gtacaataaa ctttttccat gcgattgtg acaaatttag 1050  
acatccctct ctgcacatac agaaaaactcc agcagattgt cctgtaattg 1100  
ctattgacag ctttaggcac atgtatgtgt tgggagactt caaagatgta 1150  
ttaattcctg gaaaaactca gcaattcgtt ttgacttac attctygaag 1200  
actgcacaga gaattccatc atggactga cccaactgat acagccccag 1250

gagagcaagg ccaagatgta gcaagcagtc cacctgagag ctcccttcag 1300  
 aaactagcac ccagtgaaata taggtatact ctattgaggg atcgagatga 1350  
 cctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
 cctacgtggt ggaaatagta aacctatatt ttcataatto tatgtgtatt 1450  
 ttatttttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<110> 309  
 <111> 406  
 <112> PRT  
 <113> Homo sapiens

<401> 309  
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 1 5 10 15  
 Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu  
 20 25 30  
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn  
 35 40 45  
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe  
 50 55 60  
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile  
 65 70 75  
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val  
 80 85 90  
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser  
 95 100 105  
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys  
 110 115 120  
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr  
 125 130 135  
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu  
 140 145 150  
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly  
 155 160 165  
 Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg  
 170 175 180  
 Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe  
 185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

- <210> 310
- <211> 182
- <212> DNA
- <213> Homo sapiens
- <220>
- <221> unsure
- <222> 16, 48
- <223> unknown base
- <400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
 ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
 caaacctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
 ggtcagggat cagtgaagc attggcagat ta 182

<110> 311  
 <211> 538  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 37, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
 <223> unknown base

<400> 311  
 ataggcctct ctggaagttg tccgggtgtg tggcggcggg agccggggct 50  
 gacaggacna ggtgcctctg cctggagaat cctccctctg cgtcggctcc 100  
 cggagccag ccttttctta acccaaccca acctagcccn gtcccagccg 150  
 cctcggcttg cctctgtcnc ggancccagc gtnaccatgc atcctgcctg 200  
 ctctctatcc ctaccagacc tcagatgctc cctctctctc ctggtaacct 250  
 cggctctctac cctcttaaca actgaaataa cngctcttga taccnagaat 300  
 atagatgaaa ttttaaacna tctctatctg gctcttagtca attcttatgc 350  
 tgcctgggtg cgtttcagtc agatctggca tccaattctt gaggangctt 400  
 cccatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgct 450  
 acatgtcatt gtgatcagca cctctacata gcccagagat acaggataag 500  
 caatatacca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550  
 aatccatggg tcagcgatca gtgaagcat tggcagatta catcaggc 596

<110> 312  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Synthetic oligonucleotide probe

<400> 312  
 tgcagagcct ctctggaagt tg 22

<110> 313  
 <211> 19  
 <212> DNA



<112> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<401> 313

cttagagatc agtgaaagc 19

<110> 314

<111> 19

<112> DNA

<113> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<400> 314

cccaaatgaa gtagctggc 29

<110> 315

<111> 19

<112> DNA

<113> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<400> 315

ccgcctcaaaa atgcattgtc 20

<110> 316

<111> 19

<112> DNA

<113> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<400> 316

catctggcag gaattgtcc 19

<110> 317

<111> 18

<112> DNA

<113> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<400> 317

cgtgcctatag gccaaaggc 18

<110> 318

<111> 14

<112> DNA

<113> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<217> 319

<211> 25

<213> DNA

<213> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagac 25

<217> 320

<211> 46

<213> DNA

<213> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<400> 320

cgtcttcata tctttaccgg acctcagatg ctcccttctg ctctcg 46

<217> 321

<211> 1333

<213> DNA

<213> Homo sapiens

<400> 321

ggccacgggt ccgatggggt tcaagttcgc ggccctctgc tacatgctgg 50

cgtctctgtt cactgcgcgc ctcctctctt tggccatttg gcacattata 100

gcctctgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacccccaat ccccttgtaa tcccagagta cctcctccac gcttctctct 200

gggtcaggtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

ccctctctgg catatcatat ttggagggtat atgagtagac cagtgatgag 300

tgggcacagga ctctatgacc ctacaacct catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgaaaat tagcttttta tcttctagca 400

tttttttact acctatattg catgatctat gttttggaga gctcttagaa 450

caacacacag aagaattggc ccagttaagt gcatgcaaaa agccaccaaa 500

tgaagggtatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactctta ttttttaaat gtttccacat 600

ttttgottgt ggaaagactg ttttcatatg ttatactcag ataaagattt 651  
 taaatggtat taagtataaa ttaatatata atgattacct ctggtgttga 701  
 caggtttgaa ctggcaacttc ttaaggaaca gccataatcc tctgaatgat 751  
 gcattaatta ctgaactgtcc tagtacattg gaagcttttg tttataggaa 801  
 ctgttagggc ccattttggg ttcatgaaa cagtatctaa ttataaatta 851  
 gctgtagata ccaggtgctt ctgatgaagc gaaaatgtat atctgactag 901  
 tggtaaaact catgggttcc ctcatctgtc atgtcgatga ttatatatgg 951  
 atacatttcc aaaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1001  
 ccctgtata ctgcctgaat gagagatttc ccataatttc atcagagtaa 1051  
 taaatatact tcttttaatt cttaagcata agtaaacatg atataaaaaat 1101  
 atatgotgaa ttaattgtga agaactgcatt taaagctatt ttaaattgtc 1151  
 ttttatttgc aagacattac ctattaagaa attggttatt atgcttactg 1201  
 ctctaactcg gtggttaaagg cattcttaag aatttcgagg tactacagat 1251  
 ttttaaaact gaatgagaga aaattgtata accatcttgc tgttctttaa 1301  
 ctggaatata ataaaaactct gaaattaaga ctc 1333

C110 - 332  
 C111 - 144  
 C112 - PRT  
 C113 - Homo sapiens

C110 - 332  
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu  
 1 5 10 15  
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
 20 25 30  
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
 35 40 45  
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
 50 55 60  
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
 65 70 75  
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
 80 85 90  
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
 110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
 125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser  
 140

<110> 323  
 <111> 477  
 <112> DNA  
 <113> Homo sapiens

<110> 323  
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 tgttaaaccc tgaatccct tgtactccca gactacctca tccacgcttc 100  
 ctctgtgctc atgtttcttt gtgcagcaga gtggccttaca ctgggtctca 150  
 atatgcccct ctgggcctat catattgga ggtatatgag tagaccagt 200  
 atgagtgccc caggactcta tgaccctaca accatcatga atgcagatat 250  
 tctagatcat tgcagaagg aaggatggcg caaattagct ttttatcttc 300  
 tggcaatttc ttaactacct tatggcatga tctatgtttt ggtgagctct 350  
 taaaacaaca cacagaagaa ttggtccagt taagtgcctg caaaaagcca 400  
 ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
 gantctctat agttacttta aaaaatg 477

<114> 314  
 <115> 41  
 <116> DNA  
 <117> Artificial Sequence

<118>  
 <119> Synthetic oligonucleotide probe

<120> 324  
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<121> 325  
 <122> 41  
 <123> DNA  
 <124> Artificial Sequence

<125>  
 <126> Synthetic oligonucleotide probe

<127> 325  
 ccaggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 226  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 226  
gtccagcaga gtggcttaca 20

<210> 317  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 317  
actggaccaa ttcttctgtg 20

<210> 319  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 319  
tatattctag catattgtca gaaggaagga tgggtgcaat tagct 45

<210> 319  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 319  
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ggacccaaat ggggtcccg ccgtctgtgc tctgacccat ggccctggcc 150  
ggaggttcgg ggacgcttc ggtgaagca ttgactcgg tcttgggtga 200  
taacgctct tgcacggg ccgtcagtt gaactaccc ttgcacact 250  
aacctaagga agaggagttg taagcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tcatggaatt gaattaaatc gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttgggttc cagaatcagc tgcattcgc tgaactgaga 450

caaqaacaac ttatgtccct gatgcaaaa atgcacctac tctttccctc 500  
 aac'ctgggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550  
 ccataacctc ttcctgggact ttttatcttc aagccgatga cggaaaaata 600  
 gttatattcc agtctaagcc agaaatccag taagcaccac atttgagaga 650  
 ggagcctaca aatttgagag aatcatctct aagcaaatg ccttatctgc 700  
 aaatgagaaa ttccacaagcg cacaggaatt ttcttgaaga tggagaaaag 750  
 gatggctctt taagatgctt cctctottaac ctggggtgga ttttaactac 800  
 aactcttgct cctctgggtga tgggtattgt tgggatttgt tgtgcaactg 850  
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 ggtgaactgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
 tctctctgtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
 ctatacctac aaaagtcaat cctgctcatt ctgaattta agcatttttc 1050  
 ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatagaga 1100  
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
 caataaaagt tactcaaatc tgtg 1174

<210> 330  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 330  
 Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly  
 1 5 10 15  
 Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser  
 20 25 30  
 Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr  
 35 40 45  
 Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr  
 50 55 60  
 Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg  
 65 70 75  
 Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn  
 80 85 90  
 Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser  
 95 100 105

Gln Ser Asp Glu	Gln Tyr Ala Cys His	Leu Gly Cys Gln Asn	Gln
110	115	120	
Leu Pro Phe Ala	Glu Leu Arg Gln Glu	Gln Leu Met Ser	Leu Met
125	130	135	
Pro Lys Met His	Leu Leu Phe Pro Leu	Thr Leu Val Arg Ser	Phe
140	145	150	
Trp Ser Asp Met	Met Asp Ser Ala Gln	Ser Phe Ile Thr Ser	Ser
155	160	165	
Trp Thr Phe Tyr	Leu Gln Ala Asp Asp	Gly Lys Ile Val Ile	Phe
170	175	180	
Gln Ser Lys Pro	Glu Ile Gln Tyr Ala	Pro His Leu Glu Gln	Glu
185	190	195	
Pro Thr Asn Leu	Arg Glu Ser Ser Leu	Ser Lys Met Ser Tyr	Leu
200	205	210	
Gln Met Arg Asn	Ser Gln Ala His Arg	Asn Phe Leu Glu Asp	Gly
215	220	225	
Glu Ser Asp Gly	Phe Leu Arg Cys Leu	Thr Leu Asn Ser Gly	Trp
230	235	240	
Ile Leu Thr Thr	Thr Leu Val Leu Ser	Val Met Val Leu Leu	Trp
245	250	255	
Ile Cys Cys Ala	Thr Val Ala Thr Ala	Val Glu Gln Tyr Val	Pro
260	265	270	
Ser Glu Lys Leu	Ser Ile Tyr Gly Asp	Leu Glu Phe Met Asn	Glu
275	280	285	
Gln Lys Leu Asn	Arg Tyr Pro Ala Ser	Ser Leu Val Val Val	Arg
290	295	300	
Ser Lys Thr Glu	Asp His Glu Glu Ala	Gly Pro Leu Pro Thr	Lys
305	310	315	
Val Asn Leu Ala	His Ser Glu Ile		
320			

<210> 331  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 ttgggtgata cggcgctcttg ccacggggcc tgtcagttga cctacccctt 5'  
 gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 10'  
 ggctgttttc aatttctcag tttgtggatg atggaattga cttaaatcga 15'

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaattctga 200  
 tgagcaatat gattggccatc ttgggttgcca gaatcagctg ccattcctctg 250  
 aactgagaca agaaccacctt atgtccctga tgcacaaaaat gcacctactc 300  
 tttctctataa ctctgggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 322  
 <211> 562  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 41  
 <223> unknown base

<240> 342  
 tgaactggcc ggatctttta gattcccttg accttgacca agggctcngga 30  
 aaacagcaac aagctgagct gctgtgacag agggacaacag atggcggcgcg 100  
 caaggtttagc ctttgggtga ggaaccaact ggggtcccg ccgctgctgc 150  
 tctgcaaat ggcttggcc ggaggttcgg ggaacgcttc ggcctgaagca 200  
 tttacactgg tcttgggtga taagggtct tgcacccggg cctgtcagtt 250  
 gacctacccc tgcacacct accttaagga agaggagttg taogcatgtc 300  
 aagaggttg caggctgtct ccaatttgc agttcttgga tgatggaatt 350  
 gacttaaat gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
 tccccattct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450  
 tgcatttgc tgaactgaga caagaacaac ttatgtccct gatgcacaaa 500  
 atgcactac tcttctctct aactctggtg aggtcattct ggagtgcacat 550  
 gatggattcc gc 562

<210> 343  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<240> 343  
 acacggcagc ctgctgtgac ag 22

<210> 344  
 <211> 22



<212> DNA  
<213> Artificial Sequence

<214>  
<215> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<212> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<225> Synthetic oligonucleotide probe

<410> 335  
atggcctagg ccggaggttc ggggacgcct tggctgaag 40

<210> 336  
<211> 1-85  
<212> DNA  
<213> Homo sapiens

<400> 336  
gagaggtggc gatcgctgag aggcaggagg gcggaggcgg gctcgggagg 50  
gggcacggag gtggggcgcc gctggggcgc gccgcacgg gcttcactctg 100  
agggcgcacg gcccgcgacc gagcgtcgcg actggcctcc caagcgtggg 150  
gggacaagct gccggagctg caatgggcgc ccgctgggga ttctgtttcg 200  
gctcctcggg ccgcgtgtgg ctgctcagct cgggcacagg agaggagcag 250  
cccgaggaga cagcggcaca gaggtgcttc tggcaggtta gtggttaact 300  
ggatgattgt acctgtgatg ttgaaacct tgatagattc aataactaca 350  
ggcttttccc aagactacaa aaactctctg aaagtgaata ctttaggtat 400  
taccaggtaa acctgaagag gccgtgtcct ttctgggaatg acatcagcca 450  
gtgtgggaaga agggactgtg ctgtcaaac atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctctttgaag aatgtgaaca agctgaacga ctgggagcag tggatgaatc 600  
tctgagtgag gaaacacaga aggtgtttct tcagtggaac aagcatgatg 650  
attcttcaga taactctgtg gaagctgatg acattcagtc cctgaagct 700  
gaatatgtag atttgcttct caatcctgag cgtacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga ccttttaaat ctttgggttc tggtaagg 850  
 acaagtgaag agaacccttt ttacagttgg ctagaaggtc totgtgtaga 900  
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950  
 tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggottaagaa cttgtatttc ctctaactaa 1100  
 tagaactaag ggcttttatc aaagtgttac cattcttcga ggcgccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatgtt 1200  
 actcttggaa atacttcag aaatcaagtc attcctcttg cattttgatg 1250  
 agaattcatt tttgtctgg gataaaaaag aagcacacaa actaaaggag 1300  
 gaatttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
 ttgtttttaa tgttgtctgt ggggaagct ccagaactcag ggtttgggca 1400  
 ctgtcttgaa gatcttattt ctgagaaaat tgatagcaaa tatgccagaa 1450  
 agtggaccta gttatgaatt ccacttaacc agacaagaaa tagtatcatt 1500  
 attcaagca tttggaagaa ttctacaag tgtgaaagaa ttagaaaact 1550  
 ccaggaaact gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtottaag ccaaacattt tatataaagt tgcctttgta 1700  
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aataactctg tgagtaaaag taatacttca ataactgtgt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<400> 337  
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val  
 1 5 10 15  
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
 20 25 30

Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp		
				55					40					45		
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg		
				50					45					61		
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg		
				65					71					8		
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp		
				90					48					91		
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln		
				45					111					103		
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr		
				110					115					118		
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu		
				123					121					125		
Arg	Leu	Gly	Ala	Val	Asp	Gln	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys		
				140					135					136		
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe		
				153					160					165		
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Gln	Ala	Glu	Tyr	Val	Asp		
				170					173					173		
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp		
				175					181					185		
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Gln	Glu	Asn	Cys	Phe	Lys		
				210					173					210		
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln		
				215					220					223		
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu		
				230					233					240		
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His		
				243					250					255		
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Gln		
				260					265					270		
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Gln	Phe	Gln		
				275					281					283		
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg		
				290					295					300		
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu		
				305					310					315		

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	331	335	339
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	336	340	343
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	363	370	373
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Lys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	431	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465

Asn Ile His

<210> 338  
 <211> 397  
 <212> DNA  
 <213> Homo sapiens

<214>  
 <215> unsure  
 <216> 1-1, 263, 370, 397, 426  
 <217> unknown base

<400> 338  
 gctggaaata tggatgcat ctacgagaaa ctgttttaag ccacagacaa 50  
 ttaaaaaaccc tttaaatccc ttggcttctg gtcaaggagc aagtgaagag 100  
 nacacttttt acagtttggc agaaggtctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
 caagatatct ttacaagag acctggttag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ttttatccaa agtggttacca ttcttngagc gccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450  
acttcatgaa atcaagtcac ttcttttgca tttgatgag aattcatttt 500  
tttgctg 507

<210> 339  
<211> 20  
<212> RNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 339  
aaactgacgg agctgcaatg 20

<210> 340  
<211> 21  
<212> RNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 340  
ttgtttctta atctgagcg c 21

<210> 341  
<211> 20  
<212> RNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac ttctgactgc 20

<210> 342  
<211> 16  
<212> RNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 342  
agatattcat ccactgctcc aagtcg 26

<210> 343  
<211> 25  
<212> RNA  
<213> Artificial Sequence

4220 -

4223 - Synthetic oligonucleotide probe

4400 - 343

tggttcagaaaa cagggacata tcagc 25

4210 - 344

4211 - 50

4212 - DNA

4213 - Artificial Sequence

4220 -

4223 - Synthetic oligonucleotide probe

4401 - 344

agacagagggc acagaggtgc ttctggcagg ttagtggtta cttggatgat 50

4210 - 345

4211 - 1486

4212 - DNA

4213 - Homo sapiens

4400 - 345

gggaggggtg gggggagggg gggggggagc ggtgggttgg gaggggggag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agagggcaga 100

ggattttcca tactggacag aaacagatca ggcattggaac tccccctcgt 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgcctccccct 200

ttaacctgga tgaacatcac ccacgcttat tcccagggcc accagaagct 250

gaatttggat acagtgtctt acaacatgtt gggggtggac agcgatggat 300

ctctgttggc gccccctggg atgggccttc aggcgacggg agggggggag 350

ttctctgtct cccctgtagg gggggcccac atgcccctat tgccaagggc 400

caattaggtg actaccaact gggaaattca tctcatcttg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggatttcattg 500

tgaactaagg agaggggtgt ggcagtgtct ctgaaggctc ataaaagaaa 550

aaagagaagt gtggttaagg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaacccc agaaagcaaa aggttaggtaa tgtcagggag tagttctcat 650

gcctcttcca actgggagca tgttctgagg gtgcctccc aagcctggga 700

gtactatatt cccccatccc caggcctgtg cccctctctg gtctctgtct 750

tgttgcagct ctgtcttcag ttctgggata tctgcccgtg tggatgcttc 800

atttcagcct caggggaagcc tggcacccac tgcccaacgt gagccagagg 850

aaggetgagt acctgggttcc cagaaggaga tactggglgg gaaaaagatg 900  
aggcaaaagcg gtatgatgcc tggcaaaagg cctgcatggc tatcttcatt 950  
ctacctaatt gtgcttgaaa aagctccatg ttctctaaca gattcagact 1000  
ctgggcacgg tgtgggtggc cacacctgta attctagcac ttggggaggg 1050  
aaaggtgggc agatcacttg aggtcaggag ttcaagacca gcttggccaa 1100  
catggtgaaa ctccatctct actaaaaaaa aaaaaatata aaaattagct 1150  
gggtggcgta gtgcattgct gtaactccat ctactcggga ggctaagaca 1200  
cgagaactct acctcaaccc agggagtgga ggttggggtg agccaagatt 1250  
ctgctcttgc actctagagt gggtagacaga gtaaggcaga ctccatctca 1300  
aaaaataata taataataat tcagactcct tatcaggagt ccattgatctg 1350  
gcttggccaa gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
gcaggaggat tgcctgaggt ctggaggttt gagaccagcc tgggcaacat 1450  
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<110> 346  
<111> 124  
<112> PRT  
<113> Homo sapiens

<110> 346  
Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe  
1 5 10 15  
Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro  
20 25 30  
Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val  
35 40 45  
Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala  
50 55 60  
Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg  
65 70 75  
Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His  
80 85 90  
Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn  
95 100 105  
Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly  
110 115 120

Phe Met Val Ser

<210> 347  
<211> 509  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22  
<223> unknown base

<400> 347  
cttcagttccac caccatcact cttcccatto cttcccaactt tatttttttagc 50  
ttcccatctgg gaggggggag gatggggagg aaagtgaaga aaacagaaaa 100  
atagagagagac agagggcaga ggactttctca tactggacag aaaccgatca 150  
gacatgaaac tcccccttgt cactcacttg ttcttgccac tgggtgttct 200  
gacagggtctc tgcctccctt ttaacctgga tgaacatcac ccacgcctat 250  
tccacagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300  
atagggtagac agcgatggat gctgggtggg gccccctggg atggggccttc 350  
atagagacagg aggggggagc ttctatcgtg cctgttaggg gggggccaca 400  
atgcccctatg tgccaaggga cacttaggtg actaccaact gggaaattca 450  
ctccatcttg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
ctgtgattgg 509

<210> 348  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 348  
atgagagagag gccagaggac ttc 23

<210> 349  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 349  
caggtgcata ttacagcag gatg 24



\*010 \* 350  
\*011 \* 45  
\*012 \* DNA  
\*013 \* Artificial Sequence

\*020 \*  
\*021 \* Synthetic oligonucleotide probe

\*400 \* 350  
ggactcccc ttggtccctc acctgttctt gcccctgggtg ttctt 45

\*010 \* 351  
\*011 \* 2156  
\*012 \* DNA  
\*013 \* Homo sapiens

\*400 \* 351  
aaagtacat ttctcttgga actctcctag gccactccct gctgatgcaa 5'  
catctggggtt tgggcagaaa ggagggtgct tgggagcccg cccctttctga 100  
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcactccaa catatgcatt ctgaagaaa atggctgaga tggacagaat 200  
gtttctctt ggaaagaaa aatgttctag gtcaaacctga gctaccaaa 250  
tggagaattt cacaatgggt ctagaagaaa tctggacaag ccttttctatg 300  
tggctttctt aagcattgat cccatgtttg ctccacagatg aagtggccat 350  
ctctcctgcc cctcagaacc cctctgtact ctcaaccacc atgaagcacc 400  
ctctgagtgt gagccagctg atctggcctg gagaaacagt gtactattct 450  
gtctaatacc agggggagta ccagagcctg tacaagagcc acatctggat 500  
ccctagccagc tggctgtcac tcaatgaagg ccttgagtgt gatgtcaactg 550  
atgacatcac ggcactgtg ccatacaacc ttctgttcag ggcacacctg 600  
ggctcacaga cctcagcctg ggcctcctg aagcactcct ttaatagaaa 650  
ctcaaccacc cttaccagac ctgggatgga gatcaccaaa gatggcttcc 700  
accctggttat tgagctggag gacctggggc ccaggtttga gtcctctgtg 750  
gacctactgga ggaggggagc tggctgcag gaacatgtca aaatggtgag 800  
gagtgggggt attccagtgc acctagaaa catggagcca ggggtctgat 850  
actgtgtgaa ggcacagaca ttctggaagg ccattgggag gtacagccgc 900  
ctcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccttggt 950  
actggccctg ttctcctttg ttggcttcat gctgactctt gtggtcgtgc 1000

caactgttcgt ctggaaaatg ggcgggctgc tccagtactc ctgttgcccc 1050  
 gtggtgggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100  
 aatnagctgc agaagggagg aggtggatgc ctgtgccaag gctgtgatgt 1150  
 ctcttgagga actcctcagg gcttggatct cataggtttg cgggaagggc 1200  
 cagutgaagc cgaagaacctg gtctgcatga catggaaacc atgaggggac 1250  
 aagtcgtgtt cctgttttcc gccacggaca agggatgaga gaagtaggaa 1300  
 gagctgtttg cctacaagtc tagaagcaac catcagagga aggggtggctt 1350  
 gtcataacaga acaactgactg aggtctaggg gatgtgacct ctgactggg 1400  
 ggcggccact tgcctggctga gcaacctgg gaaaagtga ttcaccttt 1450  
 aggtcctaag tttctccac tctaattggg gaattaccta cacacctgct 1500  
 aaacacacac acacagagtc cctctctata tatacacacg tacacataaa 1550  
 tacacccagc acttgcaagg cttagagggaa actggtgaca ctctacagtc 1600  
 tgaatgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
 gatcaaggac cctacacact ggggtggcttg gagagccac tttccagaa 1700  
 caatccttga gagaaaagga atcatgggag caatggtgtt gagtccactt 1750  
 caaycccaat gccggtgcag aggggaatgg cttagggagc cctacagtag 1800  
 gtgaacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850  
 accgaggatc catgaactac tctaagtgt tgcactgtg tgcacactgc 1900  
 agacagcagg tgaatgtat gctgccaatg cgaacgagaat gcagaagtca 1950  
 gtaacatgtg catgttttgt gtgctccttc tttctgttg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccacctggc caaaagcgtt aaaaaaaaaa 2050  
 aaaaaa 2056

(210) 352  
 (211) 311  
 (212) PET  
 (213) Homo sapiens

(400) 352  
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu  
 1 5 10 15  
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
 20 25 30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353  
<211> 344  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 614, 711, 745, 827  
<223> unknown base

<400> 353  
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tggacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
agaatgcctt attttgaaa gaaacaatgt totaggtcaa actgagtcta 200  
ccaatgcag actttcaca tggttctaga agaaatctgg acaagtcttt 250  
tcagtgggtt tttctacgca ttgattccat gtttgcctac agatgaagtg 300  
gcaattctgc ctgcacctca gaacctctct gtaactctca ccaacatgaa 350  
gcattctctg atgtggagcc cagtgatcgc gcttgagaa acagtgtact 400  
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tggatctcca gcagctgggt ctcaactcact gaaggctctg agtgtgatgt 500  
cactgatgac atcacggcca ctgtgcacata caacctttgt gtcagggcca 550  
cattgggtct acagacctca gcttgagca tctgaagca tccctttaat 600  
agaaactcaa ccactctac ccgacctggg atggagatca ccaaagatgg 650  
cttctcctg gttattgagc tggaggacct ggggccccag ttgagttcc 700  
ctgtggacta ntggaggagg ggogaacccc ttgoggogca aggggttngc 750  
gaacctctg cggccgtctg ggtatctctc gagaaaagag aggcccaata 800  
tgcacctcat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
gpcctctggg tgat 864

<210> 314  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 314  
aggcttctgct gcgactagac etc 23

4211 - 255  
4211 - 24  
4212 - DNA  
4213 - Artificial Sequence

4221 -  
4223 - Synthetic oligonucleotide probe

4400 - 395  
ccagtcggg caaggatggc cgag 24

4210 - 316  
4211 - 50  
4212 - DNA  
4213 - Artificial Sequence

4221 -  
4223 - Synthetic oligonucleotide probe

4400 - 316  
ttttatgca ttgattccat gtttgctcac agatgaagtg gcattctgc 50

4210 - 357  
4211 - 1070  
4212 - DNA  
4213 - Homo sapiens

4401 - 357  
ccacccagtc cgcaccagcg ccgagggaac aagagagaag agagactgaa 50  
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100  
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
ataggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200  
tggagaactg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250  
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gcttagagga gtaggaagat caggagctag agggagactg gagggctccg 350  
ggaaaataga agaggaaaag ggaaagacac agagagacgg gagagagaag 400  
agagtcgggt ttgaaggggc gatctcagtc cctggctgct ttggcatttg 450  
tggaaactgg actccctgtg gggaggagag gaaagctgga agtccctggg 500  
gtacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550  
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 tcaagggac agaatactta 1670

<110> 313  
 <111> 323  
 <112> PET  
 <113> Homo sapiens

<401> 313  
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 Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp  
 20 25 30  
 Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe  
 35 40 45  
 Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser  
 50 55 60

Leu	Cys	Ala	Val	Gly	Lys	Arg	Gln	Ser	Pro	Val	Asp	Val	Glu	Leu	65	70	75
Lys	Arg	Val	Leu	Tyr	Asp	Pro	Phe	Leu	Pro	Pro	Leu	Arg	Leu	Ser	80	85	90
Thr	Gly	Gly	Glu	Lys	Leu	Arg	Gly	Thr	Leu	Tyr	Asn	Thr	Gly	Arg	95	100	105
His	Val	Ser	Phe	Leu	Pro	Ala	Pro	Arg	Pro	Val	Val	Asn	Val	Ser	110	115	120
Gly	Gly	Pro	Leu	Leu	Tyr	Ser	His	Arg	Leu	Ser	Glu	Leu	Arg	Leu	125	130	135
Leu	Phe	Gly	Ala	Arg	Asp	Gly	Ala	Gly	Ser	Glu	His	Gln	Ile	Asn	140	145	150
His	Gln	Gly	Phe	Ser	Ala	Glu	Val	Gln	Leu	Ile	His	Phe	Asn	Gln	155	160	165
Glu	Leu	Tyr	Gly	Asn	Phe	Ser	Ala	Ala	Ser	Arg	Gly	Pro	Asn	Gly	170	175	180
Leu	Ala	Ile	Leu	Ser	Leu	Phe	Val	Asn	Val	Ala	Ser	Thr	Ser	Asn	185	190	195
Pro	Phe	Leu	Ser	Arg	Leu	Leu	Asn	Arg	Asp	Thr	Ile	Thr	Arg	Ile	200	205	210
Ser	Tyr	Lys	Asn	Asp	Ala	Tyr	Phe	Leu	Gln	Asp	Leu	Ser	Leu	Glu	215	220	225
Leu	Leu	Phe	Pro	Glu	Ser	Phe	Gly	Phe	Ile	Thr	Tyr	Gln	Gly	Ser	230	235	240
Leu	Ser	Thr	Pro	Pro	Cys	Ser	Glu	Thr	Val	Thr	Trp	Ile	Leu	Ile	245	250	255
Asp	Arg	Ala	Leu	Asn	Ile	Thr	Ser	Leu	Gln	Met	His	Ser	Leu	Arg	260	265	270
Leu	Leu	Ser	Gln	Asn	Pro	Pro	Ser	Gln	Ile	Phe	Gln	Ser	Leu	Ser	275	280	285
Gly	Asn	Ser	Arg	Pro	Leu	Gln	Pro	Leu	Ala	His	Arg	Ala	Leu	Arg	290	295	300
Gly	Asn	Arg	Asp	Pro	Arg	His	Pro	Glu	Arg	Arg	Cys	Arg	Gly	Pro	305	310	315
Asn	Tyr	Arg	Leu	His	Val	Asp	Gly	Val	Pro	His	Gly	Arg			320	325	

<210> 359

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 359  
tcgctgagg tgcagctcat tcac 24

<210> 360  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 360  
gaggtctgg aagatctgag atgg 24

<210> 361  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 361  
gctctcttgt caacttggc agtaactcta accattcct cagtgcctc 50

<210> 362  
<211> 333  
<212> DNA  
<213> Homo sapiens

<400> 362  
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gcactactg ctcaaaaag ctggggcgcc cactctggca gactaaagaa 150  
gcactcct tccacccca actgcaggtc taattttgga cgttttgct 200  
gcatttctt ccaggctgag ggagccgcag aggcggaggc tgcgtattc 250  
ctgcagtcag caccacgtc gccccggac gctcgggtgt caggccctc 300  
ggagcgggg ctctcgtct ggggtccctt gtgaaggctc tggggggctg 350  
cagaggcgg ccgtccggtt tggctcact ctccaggaa acttcacact 400  
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atctcaggt cattcattat gaagtgtacc ggcggggagt ggctcagagt 500



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catgcagagt attttggacc ttcataataa attacgaagt caggtgtatc 700  
caacagccctc taatatggag tatatgacat gggatgtaga gctggaaaga 750  
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 caaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

\*210\* 363  
 \*211\* 500  
 \*212\* PRT  
 \*213\* Homo sapiens

\*301\* 363  
 Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu  
 1 5 10 15  
 Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr  
 20 25 30

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu	
				85					40					45	
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn	
				50					55					60	
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln	
				65					70					75	
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Gln	Tyr	Met	Thr	Trp	Asp	Val	
				80					85					90	
Glu	Leu	Glu	Arg	Ser	Ala	Gln	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp	
				95					100					105	
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu	
				110					115					120	
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln	
				125					130					135	
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His	
				140					145					150	
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys	
				155					160					165	
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly	
				170					175					180	
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile	
				185					190					195	
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly	
				200					205					210	
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser	
				215					220					225	
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys	
				230					235					240	
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Gln	Gln	
				245					250					255	
Thr	Asn	Gln	Ile	Gln	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His	
				260					265					270	
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser	
				275					280					285	
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg	
				290					295					300	
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala	
				305					310					315	

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr  
330 335 339

Gln Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile  
335 340 345

Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg  
350 355 360

Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile  
365 370 375

Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr  
380 385 390

Val Gln Ala Val Thr Cys Glu Thr Thr Val Gln Gln Leu Cys Pro  
395 400 405

Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg  
410 415 420

Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr  
425 430 435

Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His  
440 445 450

Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro  
455 460 465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
485 490 495

Val Phe Ala Val Val  
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<21> 164

<21> 14

<21> DNA

<21> Artificial Sequence

<21>

<21> Synthetic oligonucleotide probe

<21> 164

ggagagatt tgggagcaca ctgg 24

<21> 165

<21> 10

<21> DNA

<21> Artificial Sequence

<21>

<21> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtctctg 20

<410> 366  
<411> 25  
<412> DNA  
<413> Artificial Sequence

<420>  
<423> Synthetic oligonucleotide probe

<440> 366  
cgcacagatt ttctctacag ccccc 25

<410> 367  
<411> 24  
<412> DNA  
<413> Artificial Sequence

<420>  
<423> Synthetic oligonucleotide probe

<460> 367  
cactatcca gcatgtactg ctgc 24

<410> 368  
<411> 30  
<412> DNA  
<413> Artificial Sequence

<420>  
<423> Synthetic oligonucleotide probe

<490> 368  
ccatttcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<410> 369  
<411> 1645  
<412> DNA  
<413> Homo sapiens

<410> 369  
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 ttcacacacag gctgcttttt atcaaaaagg ggaaaaactc tgcctttcct 800  
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 cttaaaaata tatgaataca tgogcaatac acagctacag acacacattc 1350  
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 cagtatatgc cgcattgtac tgcgtgttta tatgctatgt acatgtcaga 1600  
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(210) 370

(211) 111

(212) PRT

<213> Homo sapiens

<400> 370

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				20				25					30	
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35				40						45
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50				55						60
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65				70						75
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80				85						90
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95				100						105
Arg	Arg	Val	Tyr	Glu	Glu									
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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

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<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 372

cccccaactgg ttggagttc tccc 24

<210> 373

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

4000 373

ctcgggtcag catgaggctc ctggcgcccg ctgctcctgc tgcg 45

4010 374

4011 3113

4012 DNA

4013 Homo sapiens

4000 374

gcacacagga ctgctatgga ctcccttggt gttcaccccg gtctgggtca 50

tgtaaaactc caatgtccctc ctgtgggttaa ctgctcttgc catcaagttc 100

acccctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggctaagaa caccgttacc caatgagatc ttgggtccag 200

tggaagagta cttaggggtc ccttatgccc caccacccac tggagagagg 250

cggtctcagc ccccaagaac ccgtccctcc tggactggca ccgaaaatcc 300

tactcagttt gctgctgtgt gcccacagca cctggatgag agatccctac 350

tgcatgacat gctgcccctc tgggttaccg ccaatttggc taatttgatg 400

acccatgttc aagatcaaaa tgaagactgc cttacttaa acatctacgt 450

gcacacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgaccc tgggtgaagac gaagatattc atgacacaga cagtaagaag 550

cccgctcatgg ctatatacca tgggggatcc tacatggagg gcacccgcaa 600

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ccattcaacta ccgtctggga atactagggt ctttaagtac cggtagaccg 700

gcacacaaaag gcaactatgg gctccctggat cagattcaag cactggcggtg 750

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caactcaccg aaggctctct ccagaaggcc atcattcaga ggggcacccc 900

ccgttcacag tgggcagtga actaccagcc ggcacaagta actcggatat 950

tggcagacaa ggtcggctgc aacatgctgg acaccacgga catggtagaa 1000

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cagacgaccc ccagatcctg atggagcag gcaggttccc caactacgac 1150

atcatgctgg gctcaacca aggggaaggc ctgaagttcg tggacggcat 1200



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 cgggagacta tcaagtccat gtacacagac tgggcagata aggaaaaccc 1350  
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 agagaaggaa acgtagaaat ttattattaa aagaatggac tctgcagcga 3050  
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 taagagaact tgt 3113

#211: 375  
 #211: 316  
 #212: PRT  
 #213: Homo sapiens

#401: 375  
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 Lys Phe Thr Leu Ile Asp Ser Gln Ala Gln Tyr Pro Val Val Asn  
 20 25 30  
 Phe Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn  
 35 40 45  
 Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala  
 50 55 60  
 Ser Pro Pro Thr Gly Glu Arg Arg Phe Gln Pro Pro Glu Pro Pro  
 65 70 75  
 Ser Ser Trp Thr Gly Ile Arg Asn Thr Thr Gln Phe Ala Ala Val  
 80 85 90  
 Cys Pro Gln His Leu Asp Glu Arg Ser Leu Leu His Asp Met Leu  
 95 100 105  
 Pro Ile Trp Phe Thr Ala Asn Leu Asp Thr Leu Met Thr Tyr Val  
 110 115 120  
 Gln Asp Gln Asn Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro  
 125 130 135  
 Thr Glu Asp Gly Ala Asn Thr Lys Lys Asn Ala Asp Asp Ile Thr  
 140 145 150

Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser	
				151					160					165	
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Gln	
				170					175					180	
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly	
				185					190					195	
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly	
				200					205					210	
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu	
				215					220					225	
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Gln	Glu	Asn	Val	Gly	
				230					235					240	
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly	
				245					250					255	
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser	
				260					265					270	
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu	
				275					280					285	
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile	
				290					295					300	
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met	
				305					310					315	
Val	Gln	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Gln	Leu	Ile	Gln	Gln	
				320					325					330	
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile	
				335					340					345	
Asp	Gly	Asp	Val	Ile	Pro	Asp	Asp	Pro	Gln	Ile	Leu	Met	Glu	Gln	
				350					355					360	
Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Ile	Met	Leu	Gly	Val	Asn	Gln	Gly	
				365					370					375	
Glu	Gly	Leu	Lys	Phe	Val	Asp	Gly	Ile	Val	Asp	Asn	Glu	Asp	Gly	
				380					385					390	
Val	Thr	Pro	Asn	Asp	Phe	Asp	Phe	Ser	Val	Ser	Asn	Phe	Val	Asp	
				395					400					405	
Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Thr	Leu	Arg	Glu	Thr	
				410					415					420	
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Lys	Glu	Asn	Pro	Glu	
				425					430					435	

Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	710	715	720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys  
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp  
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg  
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr  
775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe  
785 790 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly  
800 805 810

His Ser Thr Thr Arg Val  
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<110> 376  
<111> 15  
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<113> Artificial Sequence

<220>  
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<400> 376  
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<110> 377  
<111> 15  
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<220>  
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<400> 377  
gaacccagcag ccaaaaagatg gtcac 25

<110> 378  
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<220>  
<221> Synthetic oligonucleotide probe

<400> 378  
gtacacgtgta ccaggcagca aaaggcaact atgggctcct ggatcag 47

<110> 379  
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<112> DNA

<213> Homo sapiens

<400> 379

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 ggccgcatg g 2461

<210> 330  
 <211> 343  
 <212> PRT  
 <213> Homo sapiens

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 Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu  
 20 25 30

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	
				35					40					40	
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	
				50					55					60	
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	
				65					70					75	
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	
				80					85					90	
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	
				95					100					105	
Leu	Arg	Asp	Trp	Gln	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln	
				110					115					120	
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr	
				125					130					135	
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys	
				140					145					150	
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu	
				155					160					165	
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn	
				170					175					180	
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr	
				185					190					195	
Gln	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp	
				200					205					210	
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met	
				215					220					225	
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val	
				230					235					240	
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser	
				245					250					255	
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys	
				260					265					270	
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu	
				275					280					285	
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro	
				290					295					300	
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe	
				305					310					315	



Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys  
335 340 345

Arg Phe Tyr

<210> 341

<211> 2'

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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actctccag gctgcattgt cagg 24

<210> 343

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

attcaaacatt cgagtaattg aaacggggagc actgcctgtc gaagc 45

<210> 344

<211> 1100

<212> DNA

<213> Homo sapiens

<400> 344

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ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150

tggggctctg ctcagaatc ctgcagctgg tgaaaatctg tttctagaa 200

gaggtttaat taatgootgo agtctgacat gttcccgatt tgaggtgaaa 250  
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tgotgctgct ggccctggct gogctgctgg cctttgtgag cctcagcctg 350  
cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400  
caagagtoga aagagaatca tggccgaacc tgtgaaggag cccctgtga 450  
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<210> 325

<211> 420

<212> PRT

<213> Homo sapiens

<400> 325

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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25					30

Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40					45

Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55					60

Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75

Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90

Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105

Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120

Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135

Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Gln	Ser	Pro	Leu	Asn	Ser
				140					145					150

Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Gln	Met	Gly	Glu	Leu
				155					160					165

Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180

Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
				185					190					195

Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys Ser Gly Ser	Cys Tyr Cys Pro Val	Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg	Arg Gln Tyr Leu Leu	Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr	Tyr Gly Gln Met Ala	Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu	Arg Ala Ala Asn Pro	Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His	Asn Val Ser Phe Pro	Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu	His Phe Lys Val Ile	Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu	Arg Arg Glu Lys Lys	Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala	His Pro Ile Leu Asn	Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr	Glu Gly Arg Lys Glu	Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp	Val Thr Leu Ser Pro	Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala	Arg Phe Pro Arg Phe	Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln	Asp Arg Glu Lys Pro	Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn	Gly Val Asp Val Thr	Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His	Lys Arg Ser Pro Lys	Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg	Phe Val Lys Arg Asp	Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr	Asn Tyr Tyr Asp Ala	Cys His Arg Glu Gly Phe	470	475	480

(210) 386

(211) 24

(212) DNA

(213) Artificial Sequence

(220)

(223) Synthetic oligonucleotide probe

\*400\* 386

ccaagcagct tagagctcca gacc 24

\*410\* 387

\*411\* 26

\*412\* DNA

\*413\* Artificial Sequence

\*420\*

\*423\* Synthetic oligonucleotide probe

\*400\* 387

ctctctatgc ctgtattgg catgg 25

\*410\* 388

\*411\* 37

\*412\* DNA

\*413\* Artificial Sequence

\*410\*

\*413\* Synthetic oligonucleotide probe

\*400\* 388

gacattcttg ccacatgtc agctttccct gtaccagaaa tggctgtgtt 50

\*410\* 389

\*411\* 3012

\*412\* DNA

\*413\* Homo sapiens

\*400\* 389

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atccctctctg ggagttcaag attgtgcagt aattgggttag gactctgagc 150

gcctgtgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200

cacgcgcctg aagcacaaa cagatagcta ggaatgaacc atccctggga 250

gtatgttgaa acaacggagg agctctgact tcccaactgt cccattctat 300

ggcagaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350

aattctggag gaagataaga atgattcctg cgcgaactgca cggggactac 400

aaagggcttg cctgtctggg aatcctcctg gggactctgt gggagacggg 450

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- \*210\* 330
- \*211\* 316
- \*212\* PRT
- \*213\* Homo sapiens
- \*400\* 330



Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	35
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	50
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	65
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	80
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	95
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	110
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Gln	110	115	120	125
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	140
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	155
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	170
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	185
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	200
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	215
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	230
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	245
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	260
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	275
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	290

Asp Lys Ala Ala	Gln Val Phe Lys Leu	Asp Cys Asn Ser Gly Thr	290	345	390
Ile Ser Thr Ile	Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val	Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu	Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu	Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr	Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn	Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu	Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val	Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala	Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser	Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln	Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val	Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn	Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala	Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu	Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln	Val Lys Val Met Ala	Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser	Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala	Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Gln Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Gln Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu
				875					880					885
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
				890					895					900
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro
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Ala

<110> 341

<111> 23

<112> DNA

<113> Artificial Sequence

<121>

<122> Synthetic oligonucleotide probe

<400> 341

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<110> 342

<111> 24

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<113> Artificial Sequence

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<110> 343

<111> 40

<112> DNA

<113> Artificial Sequence

<121>

<122> Synthetic oligonucleotide probe

<410> 343

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<110> 344

<111> 449

<112> DNA

<113> Homo sapiens

<410> 344

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 ctaggataag cactagatct ccttaataa actcacaact ctctgttc 999

<110> 395  
 <111> 260  
 <112> PRT  
 <113> Homo sapiens

<110> 395  
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 35 40 45  
 Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly  
 50 55 60  
 Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys  
 65 70 75

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His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Gln	Asp	His	Asn	His	Asp	
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Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	
			125						130					135	
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	
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Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Gln	
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Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Gln	Val	Lys	Ile	Phe	Pro	
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Gln	Lys	Lys	Cys	Gln	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	
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Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	
			200						205					210	
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	
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Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	
			230						235					240	
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	
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<223> Synthetic oligonucleotide probe

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<110> 337

<211> 24

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<222> Synthetic oligonucleotide probe

<400> 347

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<217> 348

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<213> Artificial Sequence

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<211> 2036

<212> DNA

<213> Homo sapiens

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<211 = 473



<212> PRT  
 <213> Homo sapiens

<400> 400

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			20						25					30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
			35						40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
			50						55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
			65						70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
			80						85					90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
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Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
			110						115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
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His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
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Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
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Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
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Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
			185						190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
			200						205					210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu
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Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
			245						250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
			260						265					270

Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu	320	325	330
Gly	Leu	Pro	Lys	Cys	Cys	Gln	Pro	Asp	Ala	Ala	Asp	Lys	Ala	Ser	335	340	345
Val	Leu	Glu	Pro	Gly	Arg	Pro	Ala	Ser	Ala	Gly	Asn	Ala	Leu	Lys	350	355	360
Gly	Arg	Val	Pro	Pro	Gly	Asp	Ser	Pro	Pro	Gly	Asn	Gly	Ser	Gly	365	370	375
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Ala	Glu	Pro	Pro	Leu	Thr	Ala	Val	Arg	Pro	Glu	Gly	Ser	Glu	Pro	395	400	405
Pro	Gly	Phe	Pro	Thr	Ser	Gly	Pro	Arg	Arg	Arg	Pro	Gly	Cys	Ser	410	415	420
Arg	Lys	Asn	Arg	Thr	Arg	Ser	His	Cys	Arg	Leu	Gly	Gln	Ala	Gly	425	430	435
Ser	Gly	Gly	Gly	Gly	Thr	Gly	Asp	Ser	Glu	Gly	Ser	Gly	Ala	Leu	440	445	450
Pro	Ser	Leu	Thr	Cys	Ser	Leu	Thr	Pro	Leu	Gly	Leu	Ala	Leu	Val	455	460	465
Leu	Trp	Thr	Val	Leu	Gly	Pro	Cys								470		

4110-401

4111-24

4211- DNA

4212- Artificial Sequence

4220-

4221- Synthetic oligonucleotide probe

4400-401

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4110-402

4111-24

4212- DNA

<213> Artificial Sequence

<216>

<215> Synthetic oligonucleotide probe

<400> 402

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<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<216>

<215> Synthetic oligonucleotide probe

<400> 403

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<211> 404

<211> 2'38

<212> DNA

<213> Homo sapiens

<400> 404

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 <212> PRT  
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 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
 50 55 60  
 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
 65 70 75  
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 80 85 90  
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 95 100 105  
 Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
 110 115 120  
 Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
 125 130 135  
 Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
 140 145 150

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Leu	Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly			
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Ser	Glu	Glu	Ile	Gly	Lys	Thr	Phe	Lys	Ile	Asn	Pro	Leu	Thr	Gly			
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				410					415					420			
Ile	Thr	Val	Thr	Asp	Leu	Gly	Thr	Pro	Met	Leu	Ile	Thr	Gln	Leu			
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455		460	465
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
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Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485		490	495
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500		505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515		520	525
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
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Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545		550	555
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560		565	570
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
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Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590		595	600
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
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Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620		625	630
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635		640	645
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
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Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665		670	675
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680		685	690
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695		700	705
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710		715	720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His  
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln  
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys  
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly  
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Asn Ile Gln

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<110> 407

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<112> DNA

<113> Artificial Sequence

<114>

<115> Synthetic oligonucleotide probe

<400> 417

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<400> 448

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<110> 419

<111> 1-79

<112> DNA

<113> Homo sapiens

<400> 499



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 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
 gajttcagag cctagcggcg tcacctgttg tggcggagga gggaggact 450  
 caaggtgcac cgtccgagag agccttttct cctctggatgg cgtcggagca 500  
 cactccctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
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 aaacggtagt gactgtactc tagtcctgtt ttacaccccg tggcgcgct 750  
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 gctcttcaat tttggcact ggatgcact cagcacagca gctctctac 850  
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 aacaaatggc cagattcaat catacagatc gaacactgga aacactgaaa 950  
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 tatgtaccca ttcgaaactg agtattcgg tggctaattc caggacaaga 1150  
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 caataagcaa atgcaaaaat attcaatag 1379

<111> 360  
 <112> PBT  
 <113> Homo sapiens

<400> 410

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				20					25					30
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
				35					40					45
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly
				50					55					60
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
				65					70					75
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His
				80					85					90
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Gln	Ala	Glu	Asp	Lys	Val
				95					100					105
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu
				110					115					120
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly
				125					130					135
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Gln	Glu	Tyr	Tyr	Thr	Glu
				140					145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
				155					160					165
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
				170					175					180
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
				185					190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Tyr
				200					205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
				215					220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
				230					235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
				245					250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly

260					265					270				
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu
				275					280					285
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys
				290					295					300
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro
				305					310					315
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu
				320					325					330
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu
				335					340					345
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu
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<210>  
 <211> Synthetic oligonucleotide probe

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<210> 412  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence

<210>  
 <211> Synthetic oligonucleotide probe

<210> 412  
 ccacacagtc ctgctatgt cctgg 25

<210> 413  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<210>  
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<210> 413  
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<210> 414  
 <211> 1136  
 <212> DNA  
 <213> Homo sapiens

0400 - 414

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gggcagcaat tgcaagccca ccccggtcaa cctgcagctg tgcacgggca 200  
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gtgcaccccg gacaccaaga agttccctgg ctgcctcttc gcccctgctt 350  
gcctcgatga cctagacgag accatccagc catgcacctc gctctgggtg 400  
caggtgaagc accgtcggc cccggtccat ccgcctctcg gcttccctcg 450  
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0210 - 415

0211 - 295

0212 - PRT

0213 - Homo sapiens

0400 - 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser

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His Cys Cys Leu Gly	Ser Ala Arg Gly	Leu Phe Leu Phe Gly	Gln
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Pro Asp Phe Ser Tyr	Lys Arg Ser Asn Cys	Lys Pro Ile Pro Val	
35	40	45	
Asn Leu Gln Leu Cys	His Gly Ile Glu Tyr	Gln Asn Met Arg Leu	
50	55	60	
Pro Asn Leu Leu Gly	His Glu Thr Met Lys	Glu Val Leu Glu Gln	
65	70	75	
Ala Gly Ala Trp Ile	Pro Leu Val Met Lys	Gln Cys His Pro Asp	
80	85	90	
Thr Lys Lys Phe Leu	Cys Ser Leu Phe Ala	Pro Val Cys Leu Asp	
95	100	105	
Asp Leu Asp Glu Thr	Ile Gln Pro Cys His	Ser Leu Cys Val Gln	
110	115	120	
Val Lys Asp Arg Cys	Ala Pro Val Met Ser	Ala Phe Gly Phe Pro	
125	130	135	
Trp Pro Asp Met Leu	Glu Cys Asp Arg Phe	Pro Gln Asp Asn Asp	
140	145	150	
Leu Cys Ile Pro Leu	Ala Ser Ser Asp His	Leu Leu Pro Ala Thr	
155	160	165	
Glu Glu Ala Pro Lys	Val Cys Glu Ala Cys	Lys Asn Lys Asn Asp	
170	175	180	
Asp Asp Asn Asp Ile	Met Glu Thr Leu Cys	Lys Asn Asp Phe Ala	
185	190	195	
Leu Lys Ile Lys Val	Lys Glu Ile Thr Tyr	Ile Asn Arg Asp Thr	
200	205	210	
Lys Ile Ile Leu Glu	Thr Lys Ser Lys Thr	Ile Tyr Lys Leu Asn	
215	220	225	
Gly Val Ser Glu Arg	Asp Leu Lys Lys Ser	Val Leu Trp Leu Lys	
230	235	240	
Asp Ser Leu Gln Cys	Thr Cys Glu Glu Met	Asn Asp Ile Asn Ala	
245	250	255	
Pro Tyr Leu Val Met	Gly Gln Lys Gln Gly	Gly Glu Leu Val Ile	
260	265	270	
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<210> 417  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 417  
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<210> 418  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 418  
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<210> 419  
 <211> 1830  
 <212> DNA  
 <213> Homo sapiens

<400> 419  
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 cgtgggtgtg tctgtctcga gatcagcctg ctcaactgct ccaacggcac 150  
 gctgtggttc agctttgcac ctgtgggtga cgtcattgct gaggacttgg 200  
 tctgttccat ggagcagatc aactggctgt cactgggtct cctcgtggta 250  
 ccaccccac ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300  
 ccgtgcyggc accatcctgg gtgctgtggt gaactttgcc gggagtgtgc 350  
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gggagcgaat tacaaggcg cactgaaaa 1830

42100 420  
 42110 560  
 42120 PRT  
 42130 Homo sapiens

43000 430  
 Met Ala Gly Pro Thr Glu Ala Glu Thr Gly Leu Ala Glu Pro Arg  
 1 5 10 15  
 Ala Leu Cys Ala Gln Arg Gly His Arg Thr Tyr Ala Arg Arg Trp  
 20 25 30  
 Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr  
 35 40 45  
 Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp  
 50 55 60  
 Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr  
 65 70 75  
 Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu  
 80 85 90  
 Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu  
 95 100 105  
 Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val  
 110 115 120  
 Gly Thr Gln Asn Pro Phe Ala Phe Leu Met Gly Gly Gln Ser Leu  
 125 130 135  
 Cys Ala Leu Ala Gln Ser Leu Val Ile Phe Ser Pro Ala Lys Leu  
 140 145 150  
 Ala Ala Leu Trp Phe Pro Glu His Gln Arg Ala Thr Ala Asn Met  
 155 160 165  
 Leu Ala Thr Met Ser Asn Pro Leu Gly Val Leu Val Ala Asn Val  
 170 175 180  
 Leu Ser Pro Val Leu Val Lys Lys Gly Glu Asp Ile Pro Leu Met  
 185 190 195  
 Leu Gly Val Tyr Thr Ile Pro Ala Gly Val Val Cys Leu Leu Ser  
 200 205 210  
 Thr Ile Cys Leu Trp Glu Ser Val Pro Pro Thr Pro Pro Ser Ala  
 215 220 225  
 Gly Ala Ala Ser Ser Thr Ser Glu Lys Phe Leu Asp Gly Leu Lys  
 230 235 240  
 Leu Gln Leu Met Trp Asn Lys Ala Tyr Val Ile Leu Ala Val Cys  
 245 250 255



Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala	Leu Leu
260	265		270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly
275	280		285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala	Leu
290	295		300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala
305	310		315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe
320	325		330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala
335	340		345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val
350	355		360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly
365	370		375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile
380	385		390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu
395	400		405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp	Trp
410	415		420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe	Ser
425	430		435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu	Gln
440	445		450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly	Gly
455	460		465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg	Ala
470	475		480
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr Ala	Arg
485	490		495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His	Pro
500	505		510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala	Thr
515	520		525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln	Ala
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545 550 555

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560

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<120>  
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<400> 411  
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<110> 412  
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<400> 412  
cgggtcaata aacctggacg ctgg 25

<110> 413  
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<400> 413  
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<110> 414  
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(210) 425  
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 (212) ERT  
 (213) Homo sapiens

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Gly Tyr Leu Phe	Leu Leu Gly Asp Cys	Gln Glu Val Thr Thr	Leu
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Thr Val Lys Tyr	Gln Val Ser Glu Glu	Val Pro Ser Gly Thr	Val
	35	40	45
Ile Gly Lys Leu	Ser Gln Glu Leu Gly	Arg Glu Glu Arg Arg	Arg
	50	55	60
Gln Ala Gly Ala	Ala Phe Gln Val Leu	Gln Leu Pro Gln Ala	Leu
	65	70	75
Pro Ile Gln Val	Asp Ser Glu Glu Gly	Leu Leu Ser Thr Gly	Arg
	80	85	90
Arg Leu Asp Arg	Gln Gln Leu Cys Arg	Gln Trp Asp Pro Cys	Leu
	95	100	105
Val Ser Phe Asp	Val Leu Ala Thr Gly	Asp Leu Ala Leu Ile	His
	110	115	115
Val Glu Ile Gln	Val Leu Asp Ile Asn	Asp His Gln Pro Arg	Phe
	120	125	130
Pro Lys Gly Glu	Gln Glu Leu Glu Ile	Ser Glu Ser Ala Ser	Leu
	140	145	145
Arg Thr Arg Ile	Pro Leu Asp Arg Ala	Leu Asp Pro Asp Thr	Gly
	155	160	165
Pro Asn Thr Leu	His Thr Tyr Thr Leu	Ser Pro Ser Glu His	Phe
	170	175	180
Ala Leu Asp Val	Ile Val Gly Pro Asp	Gln Thr Lys His Ala	Glu
	185	190	195
Leu Ile Val Val	Lys Glu Leu Asp Arg	Gln Ile His Ser Phe	Phe
	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Gln Phe Phe Leu Ser	Lys
	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg	Pro Leu Asp Tyr	Glu Lys Asn	305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly	Pro Asn	320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu	Asp Val	335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser	Gln Pro	350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile	Ala Leu	365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu	Val His	380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys	Arg Thr	395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu	Asp Arg	410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln	Asp Gln	425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile	Gln Ile	440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser	Arg Tyr	455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His	Leu Ile	470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly	Lys Val	485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val	Ala Ile	500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu	Asn Tyr	515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu	Asp Ser	530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val	Ser Leu	545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro	Val Leu	560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala	Ser Thr	575	580	585

Gly His Leu Leu Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro	599	599
Ala Gly Thr Asp Thr Pro Pro Leu Ala	Thr His Ser Ser Arg Pro	605	615
Phe Leu Leu Thr Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala	620	630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His	635	645
Leu Phe Ile Leu Asn Pro His Thr Gly	Gln Leu Phe Val Asn Val	650	660
Thr Asn Ala Ser Ser Leu Ile Gly Ser	Gln Trp Glu Leu Glu Ile	665	675
Val Val Glu Asp Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu	680	690
Leu Arg Val Met Phe Val Thr Ser Val	Asp His Leu Arg Asp Ser	695	705
Ala Arg Lys Pro Gly Ala Leu Ser Met	Ser Met Leu Thr Val Ile	710	720
Cys Leu Ala Val Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu	725	735
Phe Met Ser Ile Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr	740	750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg	755	765
Pro Gln Lys His Ile Gln Lys Ala Asp	Ile His Leu Val Pro Val	770	780
Leu Arg Gly Gln Ala Gly Glu Pro Cys	Gln Val Gly Gln Ser His	785	795
Lys Asp Val Asp Lys Glu Ala Met Met	Gln Ala Gly Trp Asp Pro	800	810
Cys Leu Gln Ala Pro Phe His Leu Thr	Pro Thr Leu Tyr Arg Thr	815	825
Leu Arg Asn Gln Gly Asn Gln Gly Ala	Pro Ala Glu Ser Arg Gln	830	840
Val Leu Gln Asp Thr Val Asn Leu Leu	Phe Asn His Pro Arg Gln	845	855
Arg Asn Ala Ser Arg Glu Asn Leu Asn	Leu Pro Glu Pro Gln Pro	860	870



Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Gln Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr  
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\*211\* 24

\*212\* DNA

\*213\* Artificial Sequence

\*220\*

\*223\* Synthetic oligonucleotide probe

\*410\* 416

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\*411\* 417

\*412\* 24

\*413\* DNA

\*414\* Artificial Sequence

\*420\*

\*423\* Synthetic oligonucleotide probe

\*430\* 417

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\*410\* 418

\*411\* 50

\*412\* DNA

\*413\* Artificial Sequence

\*420\*

\*423\* Synthetic oligonucleotide probe

\*440\* 418

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\*410\* 419

\*411\* 1037

\*412\* DNA

\*413\* Homo sapiens

\*440\* 429

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 Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe  
 50 55 60  
 Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp  
 65 70 75  
 Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val  
 80 85 90  
 Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu  
 95 100 105  
 His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe  
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 Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser  
 125 130 135  
 Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val  
 140 145 150  
 Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly  
 155 160 165  
 Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn  
 170 175 180  
 Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln

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Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
	200	205	210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
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Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Thr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
	290	295	300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu
	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
	350	355	360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
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Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu
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Lys Gln Met Ala	Pro		
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gattctc 457

4210 433

4211 20

4212 DNA

4213 Artificial Sequence

4220

4221 Synthetic oligonucleotide probe

4410 433

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4210 434

4211 21

4212 DNA

4213 Artificial Sequence

4220

4221 Synthetic oligonucleotide probe

4400 434

tccttgatta tgcagtagtc gg 22

4210 435

4211 41

4212 DNA

4213 Artificial Sequence

4220

4221 Synthetic oligonucleotide probe

4400 435

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4210 436

4211 3451

4212 DNA

4213 Homo sapiens

4401 436

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caagtatgag gtcacgggtt ccaacccaagg ccagtctctc agaaccctgg 2000  
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gcagaaaggg cttctgctct ccaggcccaa catctccac ctggatgtgg 2150  
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a 3951

0010 - 417  
 0011 - 1141  
 0012 - PRT  
 0013 - Homo sapiens

0000 - 417  
 Met Ala Gly Ala Arg Ser Arg Asp Pro Trp Gly Ala Ser Gly Ile  
 1 5 10 15  
 Cys Tyr Leu Phe Gly Ser Leu Leu Val Gln Leu Leu Phe Ser Arg  
 20 25 30  
 Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Gln  
 35 40 45  
 Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg  
 50 55 60  
 Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro  
 65 70 75  
 Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly  
 80 85 90  
 Leu Phe Ala Cys Pro Leu Ser Leu Glu Gln Thr Asp Cys Tyr Arg  
 95 100 105

Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu	Gly Val Ser Val Arg	Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala	380	385	390

Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val	
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Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly	
				410					415					420	
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly	
				425					430					435	
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser	
				440					445					450	
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser	
				455					460					465	
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His	
				470					475					480	
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu	
				485					490					495	
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg	
				500					505					510	
Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr	
				515					520					525	
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu	
				530					535					540	
Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu	
				545					550					555	
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Irp	Leu	Lys	His	Gln	
				560					565					570	
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn	
				575					580					585	
Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser	
				590					595					600	
Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
				605					610					615	
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln	
				620					625					630	
Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys	
				635					640					645	
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr	
				650					655					660	
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp	
				665					670					675	

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly	680	685	690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro	695	700	705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met	710	715	720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro	725	730	735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val	740	745	750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr	755	760	765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr	770	775	780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu	785	790	795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro	800	805	810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser	815	820	825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val	830	835	840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln	845	850	855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro	860	865	870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val	875	880	885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser	890	895	900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg	905	910	915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu	920	925	930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu	935	940	945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn	950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Gln Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

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 <212> DNA  
 <213> Artificial Sequence

<214>  
 <215> Synthetic oligonucleotide probe

<216> 438  
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<217> 439  
 <218> 24  
 <219> DNA  
 <220> Artificial Sequence

<221>  
 <222> Synthetic oligonucleotide probe

4100 + 139

gtgtgtgggg actgcaatgt agct 24

4210 + 440

4211 + 46

4212 + DNA

4213 + Artificial Sequence

4220 +

4221 + Synthetic oligonucleotide probe

4400 + 440

atctctcat gtctcccatg aggtctctat tctccacga agcctc 46

4410 + 441

4411 + 1964

4412 + DNA

4413 + Homo sapiens

4400 + 441

ggggtccggg gcagggagct gagtggacgg ctgagagcgg cggcgcgctgc 50

atcagctcca gaaagcagcg agttggcaga gcagggctgc atttcacgca 100

gacctcgga gcacagtctt ggtccacaac aagatgctca aggtgtcagc 150

gttactgtgt gtgtgtgcag cggcttgggt cagtcagtct ctgcagctg 200

cgggggggtt ggtgcagcc gggggggggt cggacggcgg taattttctg 250

gctgataaac aatggctcac cacaatctct cagtatgaca aggaagtctg 300

acagtggaac aaattccgag acgaagtaga gcatgattat ttccgcactt 350

ggagtccagg aaaaaccttc gatcaggctt tagatccagc taaggatcca 400

tgtttaaaga tgaaatgtag tggccataaa gtatgcattg ctcaagattc 450

ccaagctgca gtctgcatta gtcacgggag gttacacac aggatgaaag 500

aagca gtagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

atgcagtgcg cagtggctta tcccagccct gtttgtgggt cagatggctc 600

tacctaactct ttccagtcca aactagaata ccaggcatgt gtcttaggaa 650

aaacgatctc agtcaaatgt gaaggacatt gcccatgtcc ttccagataag 700

cccacacagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750

caggggaagtg gcaaacagat tgoggggactg gttcaaggcc ctccatgaaa 800

gtgggaagtca aaacaagaag acaaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatctgc aaggactcac ttggctggat 900

gtttaacaga cttgatacaa actatgaact gctattggac cagtcagaga 950  
 toagaagcat ctaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000  
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 aggtatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcctc 1900  
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 aaaaaaaaaa aaaa 1964

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 <212> PFT  
 <213> Homo sapiens

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 Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly  
 20 25 30  
 Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu



25										11					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					50					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Gln	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
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Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

320					325					330				
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly
				335					340					345
Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
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Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
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Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
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Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
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Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
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116

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<214>  
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<216> 444  
 <216> 18  
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<440> 444  
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<221> 445  
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<440> 445

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(210) 446

(211) 3617

(212) DNA

(213) Homo sapiens

(40) 446

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gagcggagac aacagtaact gacgcctctt tcagcccggg atcgccccag 100

cagggatggg cgacaagatc tggctgacct tcccgttgtt ccttctggcc 150

gctctgacct cggctgttgt gctggggggg gcgggcttca cacttccctt 200

cgalagcgac ttccacttta ccttcccgcc cggccagaag gactgcttct 250

accagcccat gcccctgaag gctcgttg agatcgagta ccaagtttta 300

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aaccttagtt ttggaacaaa gaaaatcaga tggagtccac actgtagaga 400

ctgaagtggg tgattacatg ttctgctttg acaatacatt cagcaccatt 450

ctcgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500

ggcacagaa caagaagatt ggaagaaata tattaactgg acagatatat 550

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ctatgggttaa tttagtggtc atgggtgggg tctcagccat ccaagtttat 750

atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaaact 800

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tgttacagtc aagaccatta atggtctctc ccaaaatatt ttgagatata 900

aaaatajgaa acaggtataa ttttaatgtg aaaattaagt cttcacttcc 950

tgtgcaagta atcctgctga tcagttgta cttagtgty taacagggaat 1000

atcttcgaga atataggttt aactgaatga agccatatta ataactgc 1050

tttcctaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100

gagtattggg cctaattgca acaccagtc gtttttaaca ggtcttatta 1150

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tcaagtacta gtaatttaac ttcatcatga atgaactata atttttaagt 2300  
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cttaaaaattt ggggtataga acccctcaac aggttagtaa tgttggatt 2400  
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 gctatgctgt tcttccatgt gaatgtcaag acatggaggg tgttcgtaat 3350  
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 agccatctta aataagcac gtattgtgag tactgatatg tatataataa 3600  
 aaattatcaa aggaaaa 3617

4010 • 447  
 4011 • 229  
 4012 • PRT  
 4013 • Homo sapiens

4400 • 447  
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala  
 1 5 10 15  
 Ala Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro  
 20 25 30  
 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys  
 35 40 45  
 Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile  
 50 55 60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Glr Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

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 <111> 23  
 <111> TGA  
 <111> Artificial Sequence

<121>  
 <121> Synthetic oligonucleotide probe

<401> 448  
 cccagcaggg ctgggcgaca aga 23

<111> 449  
 <111> 23  
 <111> TGA  
 <111> Artificial Sequence

<121>  
 <121> Synthetic oligonucleotide probe

<401> 449

gttcttcacagt ttcatatcca ata 23

<10> 450

<11> 43

<12> DNA

<13> Artificial Sequence

<20>

<21> Synthetic oligonucleotide probe

<400> 450

ccagaaggag ccagggaag ggcagccaga tcttgctggc cat 43

<10> 451

<11> 559

<12> DNA

<13> Homo sapiens

<400> 451

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gcctgcccga gtgtgtcctg gatgctgctt tctgctcca tctccctgtg 150  
ccagggtcaa ggtgaagaaa ccagaagga actgcctct ccacggatca 200  
ctctcccaa aggtcccaag gctatggct cccctgcta tgccttgctt 250  
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ccctggaaaa ctggtgtctg tgcctcagtg ggctgaggga tctctcgtgt 350  
ctccctcgtt gaggagcatt agtaacagct actcatacat ctggattggg 400  
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gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500  
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gttcaaggac tagggcaggt ggggaagtcag cagcctcagc ttggcgtgca 650  
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aaaaaaaaa 859

<10> 452

<11> 175

0012\* PRT  
 0013\* Homo sapiens

0400\* 452  
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 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
 20 25 30  
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
 35 40 45  
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser  
 50 55 60  
 Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys  
 65 70 75  
 Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser  
 80 85 90  
 Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly  
 95 100 105  
 Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp  
 110 115 120  
 Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys  
 125 130 135  
 Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser  
 140 145 150  
 Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala  
 155 160 165  
 Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp  
 170 175

0010\* 453  
 0011\* 550  
 0012\* DNA  
 0013\* Homo sapiens

0400\* 453  
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 tgggtgtgaga gacagagga gtgggcgggg accatggggg ggacggggct 100  
 cgggtctctg gagctgtgtg ttgctgcttg cggagagctg ggcggggccc 150  
 tgggtgtgata cgtctgttcg gagccacag gactgtcgga ctgtgtcacc 200  
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 cggggagata gtgtacccct tccaggggga ctccacggtg accaagtctt 300



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 cccgtgtccct gctgcaatac tgagctgtgc aatgtagacg gggcgccccc 400  
 tctgaacagc ctccactgag gggccctcac gctctccca ctcttgagcc 450  
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<210> 454  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 454  
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 20 25 30  
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 35 40 45  
 Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
 50 55 60  
 Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
 65 70 75  
 Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
 80 85 90  
 Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
 95 100 105  
 Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
 110 115 120  
 Leu Ser Leu Arg Leu  
 125

<210> 455  
 <211> 1513  
 <212> DNA  
 <213> Homo sapiens

<400> 455  
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 attttctctt tttttctccc tcttgagtc tcttgagatg atggtctctg 150  
 gccgcagcgg agctaccgg gtctttgtcg cgatggtagc gccggctctc 200

ggagggaacc ctctgtggg agtgagggcc accttgaact cggttctcaa 250  
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 acccaggctc tgcagtcagc ggcggggggg gaatctgtta cccggggggg 350  
 aataagtacc agaccattga caactaccag ccgtacccgt gcgcagagga 400  
 cgaaggagtgc ggcactgatg agtaactggc tagtccacc cggggagggg 450  
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 atgggtcagc ctatgtgctg cccggggaat tactgcacaa atggaatatg 550  
 tgtgtctctc gatcaaaaac atttcggagg agaaattgag gaaaccatca 600  
 ctgaaagcct tggtaatgat catagcacct tggatgggtt tccagaaga 650  
 accaccttgt cttcaaaaaa gtatcacacc aaaggacaag aaggttctgt 700  
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 ctgaggagaa ggtctgtctt gcgggataca gaaagatcac catcaagcca 900  
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 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000  
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 ctatggaaat cccctgtgat tgcagtcaat tactgtattg caaattctca 1150  
 gctgggcact taccgtgaaa tgcattgaaa cttttaatta tttctctaaa 1200  
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 tgattgttat ctgcactgac aaatattcta tattgaactg aagtaaatca 1300  
 ttcagctta tagtccttaa aagcataaac ctttacccca ctttaattca 1350  
 gagtcagaa cgcaggatc ctttggaatg acaaatgata ggtacctaaa 1400  
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450  
 ttaattata tttcccttta ggcgtgtgata gtttttgaaa taaaatttaa 1500  
 catctaaaaa aaaaaaaaa 1518

<210> 456

<211> 266

02120 PRT

02130 Homo sapiens

04000 446

Met	Met	Ala	Leu	Gly	Ala	Ala	Gly	Ala	Thr	Arg	Val	Phe	Val	Ala
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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser
			20						25					30

Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu
			35						40					45

Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val
			50						55					60

Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln
			65						70					75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu
			80						85					90

Cys	Gly	Thr	Asp	Gln	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp
			95						100					105

Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg
			110						115					120

Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn
			125						130					135

Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile
			140						145					150

Gln	Gln	Thr	Ile	Thr	Gln	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu
			155						160					165

Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His
			170						175					180

Thr	Lys	Gly	Gln	Gln	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys
			185						190					195

Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys
			200						205					210

Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg
			215						220					225

Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly
			230						235					240

Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser
			245						250					255

Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His				
			260						265					

<210> 457  
<211> 438  
<212> DNA  
<213> Homo sapiens

<220>  
<221> feature  
<222> 35, 123, 133, 139, 180, 214, 259, 282, 309, 452, 467, 471, 473,  
509, 556  
<223> unknown base

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ataaagtacc agaccattga caattaccag ccgtaccctt ggcagagga 400  
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<410> 458  
<411> 4040  
<412> DNA  
<413> Homo sapiens

<400> 458  
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ttctctcttg cactgggtgc ttgggctcgg ccaggcgggg tccgcgcaca 150  
gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200  
gtatatcttt gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250  
ttcacagatt aatatctttg gggacagatt tgtgatgctt gattcacctt 300

tgaagtaatg tagacagaag ttctcaaatt tgcattattac atcaacttga 350  
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gacacattctc tgtttttctga tagtgtatat ggccattttta gtggggcacag 500  
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 aagggttga aaatgctttt aatttttctc agccagagaa cagtgcagca 3350  
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 <212> PRT  
 <213> Homo sapiens

<214> 459  
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 Gly Thr Asp Gln Asp Phe Tyr Ser Leu Leu Gly Val Ser Lys Thr  
 35 40 45  
 Ala Ser Ser Arg Gln Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu  
 50 55 60  
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly  
 65 70 75

Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	
				80					85					90	
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	
				95					100					105	
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	
				110					115					120	
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	
				125					130					135	
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	
				140					145					150	
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	
				155					160					165	
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	
				170					175					180	
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	
				185					190					195	
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly	
				200					205					210	
Met	Ala	Pro	Val	Lys	Tyr	His	Gly	Asp	Arg	Ser	Lys	Glu	Ser	Leu	
				215					220					225	
Val	Ser	Phe	Ala	Met	Gln	His	Val	Arg	Ser	Thr	Val	Thr	Glu	Leu	
				230					235					240	
Trp	Thr	Gly	Asn	Phe	Val	Asn	Ser	Ile	Gln	Thr	Ala	Phe	Ala	Ala	
				245					250					255	
Gly	Ile	Gly	Trp	Leu	Ile	Thr	Phe	Cys	Ser	Lys	Gly	Gly	Asp	Cys	
				260					265					270	
Leu	Thr	Ser	Gln	Thr	Arg	Leu	Arg	Leu	Ser	Gly	Met	Leu	Phe	Leu	
				275					280					285	
Asn	Ser	Leu	Asp	Ala	Lys	Glu	Ile	Tyr	Leu	Glu	Val	Ile	His	Asn	
				290					295					300	
Leu	Pro	Asp	Phe	Glu	Leu	Leu	Ser	Ala	Asn	Thr	Leu	Glu	Asp	Arg	
				305					310					315	
Leu	Ala	His	His	Arg	Trp	Leu	Leu	Phe	Phe	His	Phe	Gly	Lys	Asn	
				320					325					330	
Glu	Asn	Ser	Asn	Asp	Pro	Glu	Leu	Lys	Lys	Leu	Lys	Thr	Leu	Leu	
				335					340					345	
Lys	Asn	Asp	His	Ile	Gln	Val	Gly	Arg	Phe	Asp	Cys	Ser	Ser	Ala	
				350					355					360	



Pro	Asp	Ile	Cys	Ser	Asn	Leu	Tyr	Val	Phe	Gln	Pro	Ser	Leu	Ala	365	370	375
Val	Phe	Lys	Gly	Gln	Gly	Thr	Lys	Glu	Tyr	Glu	Ile	His	His	Gly	380	385	390
Lys	Lys	Ile	Leu	Tyr	Asp	Ile	Leu	Ala	Phe	Ala	Lys	Glu	Ser	Val	395	400	405
Asn	Ser	His	Val	Thr	Thr	Leu	Gly	Pro	Gln	Asn	Phe	Pro	Ala	Asn	410	415	420
Asp	Lys	Glu	Pro	Trp	Leu	Val	Asp	Phe	Phe	Ala	Pro	Trp	Cys	Pro	425	430	435
Pro	Cys	Arg	Ala	Leu	Leu	Pro	Gln	Leu	Arg	Arg	Ala	Ser	Asn	Leu	440	445	450
Leu	Tyr	Gly	Gln	Leu	Lys	Phe	Gly	Thr	Leu	Asp	Cys	Thr	Val	His	455	460	465
Glu	Gly	Leu	Cys	Asn	Met	Tyr	Asn	Ile	Gln	Ala	Tyr	Pro	Thr	Thr	470	475	480
Val	Val	Phe	Asn	Gln	Ser	Asn	Ile	His	Glu	Tyr	Glu	Gly	His	His	485	490	495
Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro	500	505	510
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr	515	520	525
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro	530	535	540
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met	545	550	555
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys	560	565	570
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr	575	580	585
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln	590	595	600
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg	605	610	615
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr	620	625	630
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp	635	640	645

Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe  
650 655 660

Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val  
665 670 675

Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln  
680 685 690

Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr  
695 700 705

Glu Arg Ala Lys Arg Asn Pro Gln Glu Glu Gln Ile Asn Thr Arg  
710 715 720

Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr  
725 730 735

Leu Arg Asn Gln Gly Lys Arg Asn Lys Asp Glu Leu  
740 745

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 460

actcccccagg ctgttcacac tggc 24

<210> 461

<211> 24

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 461

ggtcagccag ccaataccag cagg 24

<210> 462

<211> 50

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 462

gttgtgatga tagaatgctt tgcgaatga aaggagtcaa cagctatccc 50

<210> 463

<211> 1818

<212> DNA

<213> Homo sapiens

<400> 463

agacagtacc tcttccctag gactacacaa ggactgaacc agaaggaaga 50  
ggacagagca aagccatgaa catcatctta gaaatcttct tgcctctgat 100  
caccatcctc tactcttact tggagtcgtt ggtgaagttt ttcattcttc 150  
agaggagaaa atctgtgggt ggggagattg ttctcattac tggagctggg 200  
catggaatag gcaggcagac tacttatgaa ctgcacaaac gacagagcat 250  
attgggttctg tgggatatta ataagcgggg tgtggaggaa actgcagctg 300  
agtgcgaaa actaggcgct actgggcctg cgtatgtggt agactgcagc 350  
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400  
tgatgtaaca atcgtgggga ataatgctgg gacagtatat ccagccgctc 450  
ctctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500  
ctaggacatt ctgggacac aaaagcactt ctccatctga tgatggagag 550  
aaatcatggc cactctgtca cagtggcttc agtgcggggc caccgaaggga 600  
ctccttacct cctcccatat tgttcacgca aatttgccgc tgttggcttt 650  
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700  
aacctcatgt ctctgcacag tttttgtgaa tactgggttc accaaaaatc 750  
caagcacaaag attatgggct gtattggaga cagatgaagt cgtagaagt 800  
ctgatagatg gaatacttac caataagaaa atgattctctg ttcctctgta 850  
tatcaatctc tttctgagac tacagaagtt tcttcttgaa cgcgcctcag 900  
cgattttaaa cgttatgcag aatattcaat ttgaagcagt ggttggccac 950  
aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcctg 1000  
ataatgatat gaatagtttc gaatcaatgc tgcaaaagctt tacttcacat 1050  
tttttcagtc ctgataatat taaaaacatt ggtttggcac tagcagcagt 1100  
caaacgaaca agattaatta cctgtcttcc tgttctctca gaatatctac 1150  
gtagtcttct ataggtctgt ttttcttct atgctcttta aaaactctct 1200  
tgcttacata aacatactta aaaggcttct tctaagatat tctatttttc 1250  
catttaaagg tgjacaaaag ctacctcctt aaaagtaaat acaaagagaa 1300  
cttattttaca caggggaaggt ttaagactgt tcaagtagca ttccaatctg 1350

tagccatgcc acagaatata aacaagaaca cagaatgagt gcacagctaa 1400  
 gagatcaagt ttcagcaggg agctttatct caacctggac atattttaag 1450  
 attcagcatt tgaagattt cctagacctt ttcctttttt attagcccaa 1500  
 aacgggtgcaa cctctattctg gactttatta ctgattcttg tcttctgtat 1550  
 aactctgaag tccacaaaaa gtggacctc tatatttctt ccttttttat 1600  
 agtcttataa gatacattat gaaagggtgac cgaactctatt ttaaattctca 1650  
 gaattttaag ttctagcccc atgataacct tttcttttgt aatttatgct 1700  
 ttcctatata ctgggtccca gagatgttta gacaatttta ggctcaaaaa 1750  
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800  
 atggacccaa gagaagaa 1818

<210> 464  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
 Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Ile Thr Ile Ile  
 1 5 10 15  
 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg  
 20 25 30  
 Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly  
 35 40 45  
 His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln  
 50 55 60  
 Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu  
 65 70 75  
 Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr  
 80 85 90  
 Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn  
 95 100 105  
 Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn  
 110 115 120  
 Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Gln  
 125 130 135  
 Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp  
 140 145 150  
 Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly

155	160	165
His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro 170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe 185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly 200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe 215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp 230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys 245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln 260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln 275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys 290	295	300

<210> 465  
 <211> 1547  
 <212> DNA  
 <213> Homo sapiens

<400> 465  
 tggggggggg tggggggggg aggtgagggg ggggaggtga ggggggggag 50  
 ttccacagca ggaagggggg ggtgtgaggg aaggtgaagt gagagggggg 100  
 gagagggggg aggggggggg gggcaggatg accaaggggg ggtgtgttgg 150  
 gatggggggt gtgtgtgggt ggtgtgttat gatgtgtgt atcattgtgt 200  
 actgggacag ggcagggggg gggcacttct acttgacacg gtcctttctt 250  
 aggtggacac gggggggggg ggtggggggg gggggggggg acaggggacag 300  
 gaggttcag ggcgacttgg atgtggagga gtttctggag aagtttttca 350  
 gtgtgtgggt gaagcagagg gacgttttca gaaggagag ggagcagggg 400  
 cctggggggg ggagcagga ggagaggggt agagggtacg actgggttgg 450  
 ggagcagggg gggggggggg gagggggggg gggggggggg ggggggggga 500  
 ggaggtgtgt ggggggttgc tgggggaact ccaggtgtgg cttcccccac 550

aaggagcgcg cattcgacga catccccaac tgggagctga gccacctgat 600  
cgtggacgac cggcaaggcg ccatactactg ctacgtggcc aaggtgggct 650  
gcaccaactg gaagcgcgctg atgatacttg cgagcggaag cctgctgcac 700  
cgcggtggcg cctaccgaga cccgctggcg atcccgcgcg agcacgtgca 750  
caacgcacgc ggcacactga cctccaacaa gttctggcgc cgtacaggga 800  
agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagtto 850  
ctcttcgtgc ggcacccctt cgtgcgcctg atctccgctt tcgcagcaca 900  
gttcgagctg gagaacgagg agttctacgc caagttcgcc gtgcacatgc 950  
tcgggtctga cgcacaacac accagcctgc ccgcctcgcc ggcgcaggcc 1000  
tcgcgcctg gcctcaaggt gtccctcgcc aacttcaccc agtacctgct 1050  
ggacccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100  
tgtacccgct ctgcaccccg tgcagatcg actacgaatt cgtggggaag 1150  
ctggagaact tggacgagga cgcgcgcag ctgctgcagc tactccaggt 1200  
ggacgggcag ctccgcttcc ccccgagcta ccggaacagg accgcacgca 1250  
gtcgggagga ggaactggtt gcccaagatcc cctgggctg gaggcagcag 1300  
ctgtataaac ctacgagcg cgaacttggt ctcttcggct accccaagcc 1350  
cgaaaaactc ctccgagact gaaagcttcc gcttgctt ctctcgctg 1400  
cctggaaact gaagcagcg cactccagtt ttttatgac ctacgatttt 1450  
gcaatcggg cttctgttc actccactgc ctctatcat tgagtactgt 1500  
atcgatattg tttttaaga ttaatatatt tcaggtattt aatacga 1547

#210 - 466  
#211 - 414  
#212 - PRT  
#213 - Homo sapiens

#400 - 466  
Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser  
1 5 10 15  
Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly  
20 25 30  
Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr  
35 40 45  
Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu  
50 55 60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser			
				75					71					75			
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln			
				80					85					90			
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp			
				95					100					105			
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln			
				110					115					120			
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser			
				125					130					135			
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro			
				140					145					150			
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala			
				155					160					165			
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg			
				170					175					180			
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro			
				185					190					195			
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala			
				200					205					210			
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys			
				215					220					225			
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys			
				230					235					240			
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe			
				245					250					255			
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe			
				260					265					270			
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro			
				275					280					285			
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe			
				290					295					300			
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu			
				305					310					315			
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His			
				320					325					330			
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu			
				335					340					345			

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp  
410

<110> 467  
<111> 1071  
<112> DNA  
<113> Homo sapiens

<100> 467  
tcggggccaga attcgggcacg aggggggcacg aggggggcacg cctcacgggg 50  
attcgggaggt gaaagagggc cagagtagag agagagagag accgacgtac 100  
acgggatggc taagggaacg cgttatggc ggaaggtggt ggtcgtgacc 150  
aggggggggg ggggcacgg agcggggac gtggggggt cgtggaacag 200  
cggggcccca gtgggttatct ggcacaagga tgagtctggg ggccggggcc 250  
tggagcagga gtcacctgga gctgtcttta cctctgtga tgtgactcag 300  
gaagatgatg tgaagacccg ggtttctgag accatccggc gattcgggc 350  
cctggattgt gtgtcaca caagctggca ccaccaccc ccacagaggg 400  
ctgaggagac ctctgcccag ggattccggc agctgctgga gctgaaacct 450  
ctggggacgt acaccttgac caagctggc ctccctacc tggggaagag 500  
tcaagggaat gtcatcaaca tctccaggt ggtgggggca atcggccagg 550  
ccagggcagt tccctatgtg ggcaccaagg gggcagtaac agccatgacc 600  
aaagctttgg cctgggatga aagtcacat ggtgtccgag tcaactgtat 650  
ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700  
tgcacagacc tagggccaca atccgagagg gcctgctggc ccagccactg 750  
tgcgcgatgg gccagcccg tgaggctggg gctgcccag tgttccctgg 800  
ctccgaagcc aactctgca cgggcattga actgctcgtg acgggggggtg 850  
cagagctggg gtacgggtgc aaggccagtc ggagcaccac cgtggacgac 900



cccgatatcc cttcctgatt tctctcattt ctacttgggg ccccttctct 950  
 aggaactctcc caccaccaaac tccaacctgt atcagatgca gcccaccaagc 1000  
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcagggtc 1050  
 ccataaaaaa gatttgacgc c 1071

<210> 468  
 <211> 270  
 <212> PRT  
 <213> Homo sapiens

<400> 468  
 Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr  
 1 5 10 15  
 Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val  
 20 25 30  
 Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly  
 35 40 45  
 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu  
 50 55 60  
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu  
 65 70 75  
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala  
 80 85 90  
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln  
 95 100 105  
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr  
 110 115 120  
 Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn  
 125 130 135  
 Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln  
 140 145 150  
 Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr  
 155 160 165  
 Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn  
 170 175 180  
 Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu  
 185 190 195  
 Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met  
 200 205 210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

-C10 - 469  
 -C11 - 637  
 -C12 - DNA  
 -C13 - Homo sapiens

-C10 - 469  
 aggggggag cagctgcagg ctgaccttgc agcttggggg aatggactgg 50  
 cctcacaacc tctgtttctt ccttaccatt tcttctttcc tggggctggg 100  
 ccagcccagg agcccacaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 cctggcccc tggcctcac caggtgcac tggactggt gtcacggatg 200  
 aaacoytatg cccgcctgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcacagctg aggaacagct cagagctggc ccagagaaaag tctgaggtca 300  
 ccttgagct gtggatgtcc aacaagagga gctgtctccc ctggggctac 350  
 agcatcaacc acgacccag ccttatccc gtggacctgc cggaggccag 400  
 ggcctgtgt ctgggtgtg tgaacccctt caccatgcag gaggacccca 450  
 gcatggtgag cgtgcgggtg tccagccagg ttcctgtggg ccgcctcttc 500  
 tgcctgcac cgcctccac agggccttgc cgcacggcg cagtcctgga 550  
 naccatcgct gtgggtgca cctgcattt ctgaatcacc tggccagaaa 600  
 ggcaggccag cagcccgaga ccatctctt tgcactttg tgccagaaa 650  
 ggcctatgaa aagtaaacac tgacttttga aagcaag 637

-C10 - 470  
 -C11 - 130  
 -C12 - FET  
 -C13 - Homo sapiens

Met	Asp	Trp	Pro	His	Asn	Leu	Leu	Phe	Leu	Leu	Thr	Ile	Ser	Ile
1				5					10					15
Phe	Leu	Gly	Leu	Gly	Gln	Pro	Arg	Ser	Pro	Lys	Ser	Lys	Arg	Lys
				20					25					30

Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val
				35					40					45
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
				50					55					60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65					70					75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80					85					90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
				95					100					105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
				110					115					120
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
				125					130					135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
				140					145					150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
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Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
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 <212> DNA  
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 aaggtagatg ctattcaaga accaggtctg agtggccgct tctttgtcac 450  
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
 50 55 60  
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
 65 70 75  
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
 80 85 90  
 Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val  
 95 100 105  
 Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg  
 110 115 120  
 Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile  
 125 130 135  
 Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys  
 140 145 150  
 Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser  
 155 160 165

Ile Ser Gly Lys	Ile Trp His Leu His	Asn Tyr Phe Thr Val Thr
170	175	180
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr	Val Phe Phe Val Ile Ala
185	190	195
Thr Leu Val Phe	Gly Leu Phe Met Gly	Leu Val Leu Val Val Ile
200	205	210
Ser Gln Cys Phe	Tyr Val Pro Leu Pro	Arg His Leu Ser Glu Arg
215	220	225
Ser Gln Gln Asn	Arg Arg Ser Glu Glu	Ala His Arg Ala Glu Gln
230	235	240
Leu Gln Asp Ala	Gln Glu Glu Lys Asp	Asp Ser Asn Glu Glu Glu
245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp Glu	Gln Glu Lys Glu Asp Leu
260	265	270
Gly Asp Glu Asp	Gln Ala Glu Glu Glu	Gln Glu Glu Asp Asn Leu
275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser	Gln Ala Asn Asp Gln Gly
290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg	Gln Glu Val Glu Pro Glu
305	310	315
Gln Ala Glu Glu	Gly Ile Ser Glu Gln	Pro Cys Pro Ala Asp Thr
320	325	330
Gln Val Val Glu	Asp Ser Leu Arg Gln	Arg Lys Ser Gln His Ala
335	340	345
Asp Lys Gly Leu		

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 c2170 DNA  
 c2171 Artificial Sequence

c2200  
 c2201 Synthetic oligonucleotide probe

c2202 473  
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c2210 474  
 c2211 24  
 c2212 DNA  
 c2213 Artificial Sequence

c2220

<123> Synthetic oligonucleotide probe

<400> 474

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<110> 475

<111> 44

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<113> Artificial Sequence

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<400> 475

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<110> 476

<111> 2473

<112> DNA

<113> Homo sapiens

<400> 476

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atatactcaa ttacacttcg actctcaaaag caataccagg atagctgttg 250

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 <211> 201  
 <212> PRT  
 <213> Homo sapiens

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 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu  
 35 40 45  
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile  
 50 55 60  
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro  
 65 70 75  
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met  
 80 85 90  
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu  
 95 100 105  
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe  
 110 115 120  
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile  
 125 130 135  
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp  
 140 145 150  
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala  
 155 160 165  
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser  
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<210> 478

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+2112+ DNA  
+2113+ Artificial Sequence

+22+  
+223+ Synthetic oligonucleotide probe

+400+ 473  
gtccacagac agtcattcca ggagcag 27

+210+ 479  
+211+ 20  
+212+ DNA  
+213+ Artificial Sequence

+220+  
+223+ Synthetic oligonucleotide probe

+400+ 479  
acaagtgctc tcccaacctg 20

+210+ 480  
+211+ 24  
+212+ DNA  
+213+ Artificial Sequence

+220+  
+223+ Synthetic oligonucleotide probe

+400+ 480  
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+210+ 481  
+211+ 31  
+212+ DNA  
+213+ Artificial Sequence

+220+  
+223+ Synthetic oligonucleotide probe

+400+ 481  
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+210+ 482  
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+212+ DNA  
+213+ Homo sapiens

+400+ 482  
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 <211> 693  
 <212> PRT  
 <213> Homo sapiens

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 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser  
 35 40 45  
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn  
 50 55 60  
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His  
 65 70 75  
 Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe  
 80 85 90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	105
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Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110
				110					115						
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125
				125					130						
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140
				140					145						
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155
				155					160						
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Gln	Leu	Lys	170
				170					175						
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185
				185					190						
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200
				200					205						
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215
				215					220						
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230
				230					235						
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245
				245					250						
Gln	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260
				260					265						
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Gln	Ala	Gln	275
				275					280						
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290
				290					295						
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305
				305					310						
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320
				320					325						
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335
				335					340						
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350
				350					355						
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365
				365					370						

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val	380	385	390
Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu	395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val	410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg	425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu	440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro	455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile	470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu	485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr	500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly	515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp	530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly	545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser	560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn	575	580	585
Met Ala Met Leu Ala Thr Met Val Val Glu Ile Leu Arg Leu Arg	590	595	600
Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu	605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe	620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile	635	640	645
Ile Thr Ser Phe Glu Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser	650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

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<211> 516  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 64, 70, 84, 147  
<223> unknown base

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ctgctgttgg ccgtcttctt gctggacaag agcttcttgc ccagcgnaga 150  
ccgtggcctt gacaggctct gaaggctggc tgcagagcca gtgcctctt 200  
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aactactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350  
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tgtgcatagg actccagagg ggtcctctta ccttccatg tcttggatcc 450  
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ttctgttca acatgg 516

<210> 485  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 485  
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<210> 486  
<211> 24  
<212> DNA



<013> Artificial Sequence

<020>

<003> Synthetic oligonucleotide probe

<040> 436

tgaggacta gatggggctg gacg 24

<000> 437

<001> 2849

<002> DNA

<003> Homo sapiens

<000>

<001> unsure

<002> 2715

<003> unknown base

<000> 437

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agaggggctc taggaaaaag ttttggatgg gattatgtgg aaactaccct 150

gggtttctct gctggcagag caggctcggc gcttcacccc cagtgcagcc 200

ttccctcggc ggtgggtgaaa gagaactcggg agtcgctgct tccaaagtgc 250

cggccgtgag tgagctctca cccagtcag ccaaatgagc ctcttcgggc 300

ttctctctgt gacatctgcc ctggccgggc agagacaggg gactcagggc 350

gaatccaccc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400

cggagtcacaa gatccctcagc atgagagaat tattactgtg ctactaatg 450

gaagtattca cagcccaagg tttctcaca ctatcccaag aaatacgggc 500

ttggtatgga gattagtagc agtagaggaa aatgtatgga tacaacttac 550

gtttgatgaa agatttgggc ttgaagaccc agaagatgac atatgcaagt 600

atgatittgt agaagttgag gaaccacgtg atgggaactat attagggggc 650

tgggtgtggtt ctggtaactgt accaggaaaa cagatttcta aaggaaaatca 700

aattangata agattttgtat ctgatgaata tttcccttct gaaccagggc 750

cttgcatcca ctacaacatt gtcattgcac aattcacaga agctgtgagt 800

ccctcagtgc taccoccttc agctttgcca ctggacctgc ttaataatgc 850

tataactgac tttagtaact tgggaagacat tattcgatat ctggaaccag 900

agagatggca gttggactta gaagatctat ataggccaac ttggcaactt 950

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 cagtgtccat aagggaagaa ctaaagagaa ccgataccat tttctggcca 1100  
 ggttgtctcc tgggttaaag ctgtggtggg aactgtgctt gttgtctcca 1150  
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 acgaggtcct ccagctgaga ccaaagaccg gtgtcagggg attgcacaaa 1250  
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 tggaatagaa ttggtaaagt gcaagactt tttgaaaata attaaattat 2350  
 catatcttcc attcctgtta ttggagatga aaataaaaag caacttatga 2400

aagtagacat tcagatccag ccattactaa cctattcctt ttttggggaa 2450  
atctgagcct agctcagaaa aacataaagc accttgaaaa agaactggca 2500  
gttctctgat aaagcgtgct gtgctgtgca gtaggaacac atcctattta 2550  
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aaaaaaaaaa aaaaaaaa aggtttaggg ataacagggg aatggggcc 2849

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<211> 345  
<212> PRT  
<213> Homo sapiens

<400> 488  
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Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln  
35 40 45  
His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser  
50 55 60  
Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp  
65 70 75  
Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe  
80 85 90  
Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys  
95 100 105  
Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu  
110 115 120  
Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser  
125 130 135  
Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe  
140 145 150  
Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro  
155 160 165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Val Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

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<210> 21

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<210> Artificial Sequence

<220>

<220> Synthetic oligonucleotide probe

<300> 489

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<310> 420

<311> 40

<311> DNA

<311> Artificial Sequence

<320>

<320> Synthetic oligonucleotide probe

<400> 420

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<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 491

caaccacagg ttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 492

acacacaggca cagttccccc 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

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<221> Synthetic oligonucleotide probe

<400> 493

gggggaatcc aacctgagta g 21

<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

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gggacctatcc tctgtgctc 20

<210> 495

<211> 3293

<212> DNA

<213> Homo sapiens

<400> 495

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gacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

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 aacatagaaa tactctacct gggccaaaaa tgttattatc gaaatccttg 650  
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 <111> 1049  
 <112> PRT  
 <113> Homo sapiens

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 Phe Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe  
 20 25 30  
 Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn  
 35 40 45  
 His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
 50 55 60  
 Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
 65 70 75  
 His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
 80 85 90  
 Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
 95 100 105  
 Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
 110 115 120  
 Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
 125 130 135  
 Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
 140 145 150  
 Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
 155 160 165  
 Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
 170 175 180  
 Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
 185 190 195



Glu Lys Asp Ala Phe Leu Asn Leu Thr	Lys Leu Lys Val Leu Ser	201	215	211
Leu Lys Asp Asn Asn Val Thr Ala Val	Pro Thr Val Leu Pro Ser	216	220	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn	Asn Met Ile Ala Lys Ile	230	235	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn	Gln Leu Gln Ile Leu Asp	245	250	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr	Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu	Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val	Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp	Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn	Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu	Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln	Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu	Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu	Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu	Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu	Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser	Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe	Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val	Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser	Cys Arg Phe Lys Asn Lys	470	475	480

Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	485	490	495
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	500	505	510
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	515	520	525
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	530	535	540
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	545	550	555
Leu	Leu	His	Ser	Thr	Ala	Phe	Gln	Glu	Leu	His	Lys	Leu	Glu	Val	560	565	570
Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile	575	580	585
Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys	590	595	600
Leu	Met	Met	Asn	Arg	Asn	Asp	Ile	Ser	Ser	Ser	Thr	Ser	Arg	Thr	605	610	615
Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly	Asn	His	620	625	630
Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn	Arg	Tyr	Leu	Gln	Leu	635	640	645
Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp	Ile	Ser	Lys	Asn	650	655	655
Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly	Met	Pro	Pro	665	670	675
Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	Ser	Phe	680	685	690
Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp	695	700	705
Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn	710	715	715
Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	725	730	735
Arg	Ser	Leu	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	740	745	745
Tyr	Leu	Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	755	760	765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val	1040	1045	

4010 - 497  
4011 - 4199  
4012 - DNA  
4013 - Homo sapiens

4400 - 497  
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<211> 1041

<212> PRT

<213> Homo sapiens

<400> 493

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Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
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Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
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Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
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Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
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Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
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Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
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Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
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Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
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Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
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Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly	Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser Gly	245	250	255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro Cys	260	265	270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln Asn	275	280	285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu Arg	290	295	300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys Val	305	310	315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser Gly	320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu Ser	335	340	345
Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile Ser	350	355	360
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu Arg	365	370	375
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro Leu	380	385	390
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn Phe	395	400	405
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn Leu	410	415	420
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val Lys	425	430	435
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg His	440	445	450
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Gln Phe Asp Pro His Ser	455	460	465
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys Ala	470	475	480
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe Phe	485	490	495
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys Leu	500	505	510
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr Glu	515	520	525



Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr	Asn Asn	530	535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp	545	550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile	560	565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn	575	580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr		590	595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val Phe		605	610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn Arg		620	625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu Asp		635	640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu		650	655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met		665	670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu		680	685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp		695	700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser		710	715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val		725	730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr		740	745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser		755	760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile		770	775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile		785	790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg		800	805	810

Gly	Lys	Ser	Ile	Val	Ser	Leu	Glu	Leu	Thr	Thr	Cys	Val	Ser	Asp	
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Val	Thr	Ala	Val	Ile	Leu	Phe	Phe	Phe	Thr	Phe	Phe	Ile	Thr	Thr	
				830					835					840	
Met	Val	Met	Leu	Ala	Ala	Leu	Ala	His	His	Leu	Phe	Tyr	Trp	Asp	
				845					850					855	
Val	Trp	Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Val	Lys	Gly	Tyr	
				860					865					870	
Arg	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser	
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Tyr	Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu	
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Leu	Arg	Tyr	His	Leu	Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu	
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Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val	
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Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe	
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Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile	
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<210> 501  
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•(213)• Homo sapiens

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35 40 45  
Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60  
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75  
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90  
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105  
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120  
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135  
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Glu  
140 145 150  
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu

155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys Gly	
170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro	Thr Gly Val Asp Ser Ala	
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln	Ser Arg Val Asp Leu Leu	
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala	Pro Leu His Ser Leu Ala	
215	220	225
Ser Gln Ala Leu Gln His Gly Leu Pro	Asp Pro Gly Ser Leu Leu	
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser Glu	
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys Lys	
260	265	270

Lys Asp Ser

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
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 ccaccatggc cagcctggg ctccagcagc atcagagcag cccctgtggt 150  
 tggcagcaaa gtccagcttg gctgggcccg ctgtgagggg cttcgcgcta 200  
 ggcctggcg tgtccaggg gctgaggtct cctcatcttc tccctagcag 250  
 tggatgagca acccaacggg ggcccgggga gggjaactgg ccccgaggga 300  
 gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350  
 gctgcccaca ggacggggga ggcacaggtg gcccccacca cccggaggag 400  
 cagctcctgc cctgtccgg gggatgaactg attctctctc ggcaggccac 450  
 ccagaggaga agggcacc cctgtgagga acaggcctg aggggctctc 500  
 aggaggtgct gctgatgtgg cttctggtgt tggcagtggg cggcacagag 550  
 cagcctacc ggcccggcg taggggtgtg gctgtccggg ctccgggga 600  
 cctgtctctc gactgttctg tgcagcgtgt gtaccagccc ttctcacca 650

cctgcgacgg gcaccgggac tgcagcaact accgaaccat ctataggacc 700  
 gcc'acggcc gcagccctgg gctggccact gccaggccct gctacggctg 750  
 ctgccccggc tggaagagga ccagcggggt cctcggggcc cgtggagcag 800  
 caatattcca gcggccatgc cgggaacggag ggagctgtgt ccagcctggc 850  
 cgtcgcggct gccctgcagg atggcggggc gacacttgcc agtcagatgt 900  
 ggangaatgc agtgcctagga gggcgggctg tccccagcgc tgcattcaaa 950  
 ccgtcggcag ctactgggtg cagtgttggg aggggcacag cctgtctgca 1000  
 gacggctaac cctgtgtgac caaggcaggc cccccagggc tggcccccaa 1050  
 ccgacacgga gtggacagtg caatgaaggc agaaptgcag aggcctgcagt 1100  
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 cctcctgggt cactccttcc agcagctcgg ccgcctcgac cccctgagcg 1250  
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<210> 508  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 508  
 Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
 1 5 10 15  
 Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
 20 25 30  
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
 35 40 45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	85
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	115
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	145
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Gln	155	160	165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	215	220	225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	230	235	240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	245	250	255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	260	265	270

Lys Asp Ser

<110> 519  
 <111> 1533  
 <112> DNA  
 <113> Homo sapiens

<110> 519  
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 ggggccaaca tggccaagcc tgggtccag cagcatcagc agcccccagg 200  
 accggggagg cacagggtgg ccccaaccac cggaggagca gctcctggcc 250  
 ctgtccgggg gatgaatgat tctcctccgc caggccaccc agaggagaa 300  
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 cccggccgta ggggtgtgtg tgtccgggtc cccggggacc ctgtctccga 450  
 gtcttctgtc cagcgtgtgt accagccctt cctcaccacc tgggacgggc 500  
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 gaaggaggac agcgggcttc ctggggcctg cggagcagca atatgccagc 650  
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 caccctgggc tacccccacc ctggctaccc caacggcatc ccaaggccag 1400  
 gtggggccctc agctgaggga aggtacagac tccctgttgg agcctgggac 1450  
 ccacggcaca ggcaggcag cccggaggct ggggtggggc tcagtggggg 1500

ctgctgctg acccccagca caataaaaaat gaaaogtg 1538

<110> 510  
<110> 273  
<110> PRT  
<110> Homo sapiens

<400> 510  
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
1 5 10 15  
Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
20 25 30  
Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45  
Ile Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60  
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75  
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90  
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105  
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120  
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135  
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150  
Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
155 160 165  
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
170 175 180  
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
185 190 195  
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
200 205 210  
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
215 220 225  
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
260 265 270

Lys Asp Ser

<210> 511  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 511  
Tggagagaca atatgacaga c 21

<210> 512  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 512  
ttttccactc ctgtcgggtt gg 22

<210> 513  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 513  
tggtgacatt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514  
<211> 1690  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1039-2065  
<223> unknown base

<400> 514  
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cagacgtgat tccctgggac ggtccgtttc ctgcctcag ctgcctggccg 150  
 agttgggtct ccgtgtttca ggcctggctcc ccttccctgg tctcccttct 200  
 ccctgtgggc cgttttatcg ggagagagatt gtcttcacag gctagcaatt 250  
 ggaattttga tgatgtttga ccacagcggca ggaatagcag gcaacgtgat 300  
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 cactttggag caggaattcc aatcatgtct gtgatggcgg tgagaaaagaa 400  
 ggtgacacgg aaatgggaga aactccacag caggaacacc ttttgcctgt 450  
 atggcccgct catgatggcc cggcaaaaag gcattttcta cctgacccct 500  
 ttcctcctcc tggggacatg tacactcttc ttcgcctttg agtgcctgta 550  
 ccctgctgtt cagctgtctc ctgcacacc tctatttctt gccatgctct 600  
 tctttctctc catgggtaca ctgttgagga ccagcttcag tgacccctga 650  
 gtgattcttc gggcgctacc agatgaagca gcttcctatg aaatggagat 700  
 agaagctacc aatggcgagg tgcctccagg ccagcgacca ccgctcctga 750  
 tcaagaattt ccagataaac aaccagattg tgaaactgaa atactgttac 800  
 acatgcaaga tcttcctggc tccctgggcc tccatttga gcactctgta 850  
 caactgtgtg gagcgtctcg accatcactg cccctgggtg gggcaattgt 900  
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 ctctcaccaa tctatgtctt cgtcttcaac atcgtctatg tggcctcaca 1000  
 atctttgaaa attggctctt tggagacatt gaaagaaact cctggaaactg 1050  
 ttctagaagt cctcatttgc tctttcacac tctggtccgt cgtgggaactg 1100  
 actggatttc atacttctct cgtggctctc aaccagacaa ccaatgaaga 1150  
 catcaaaagg ccatggacag ggaagaatcg cgtccagaat cctacagcc 1200  
 atggcaatat tctgaagaac tctgtggaag tctgtgtgg ccccttgccc 1250  
 ccagctgtgc tggatcgaag ggttatcttg ccactggagg aaagtggaag 1300  
 tcgacctccc agtactcaag agaaccagtag cagctctctg ccacagagcc 1350  
 cagccccacc agaaccctg aactcaaatg agatgcctga ggacagcagc 1400  
 actcccgaaag agatgcaccc tccagagccc ccagagcccac cacaggaggc 1450  
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 taattagggc tatgagagat ttcaggtgag aagttaaac tgagacagag 1550

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 caaggcagtg gcagaagatg ttagtcacct ctgataactg gaaaaatggg 1700  
 tctcttgggc ccctggcactg gttctccatg gcttcagcca caggggtccc 1750  
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 agctgctgca cgtgctgagt ccagaggcag tcacagagac ctctggccag 1900  
 gggatccctaa ctgggttctt ggggtcttca ggactgaaga ggaggagag 1950  
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 caggcaatggc agtaataaaa gtctgcactt tggcatttc ttttccctag 2150  
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 aggtctgcag aggccttgaa tgcacaaatg ggaaaccaag gcacagagag 2250  
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 cagtcagctc tgcctaggac ctgctctatt tcagggaaga agatttatgt 2550  
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 ccagggtcct gtctggatga cttatgggtt gggggagtgt aaaccggaac 2650  
 ctttcattca tctgaaggcg attaaactgt gtctaattga 2690

<210> 315  
 <211> 364  
 <212> PRT  
 <213> Homo sapiens

<400> 315  
 Met Ser Val Met Val Val Arg Lys Lys Val Thr Arg Lys Trp Glu  
 1 5 10 15  
 Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met

20					25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile
				35					40					45
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu
				50					55					60
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu
				65					70					75
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp
				80					85					90
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile
				95					100					105
Gln	Met	Glu	Ile	Gln	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln
				110					115					120
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile
				125					130					135
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro
				140					145					150
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe
				155					160					165
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn
				170					175					180
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr
				185					190					195
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser
				200					205					210
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr
				215					220					225
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val
				230					235					240
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr
				245					250					255
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val
				260					265					270
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu
				275					280					285
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly
				290					295					300
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln

305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln	Ser Pro Ala Pro Thr Glu	
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu	Asp Ser Ser Thr Pro Glu	
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu	Pro Pro Gln Glu Ala Ala	
350	355	360
Glu Ala Glu Lys		

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 86, 88, 89, 118, 135, 193, 213, 222  
 <223> unknown base

<300> 516  
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 ttgggtttg gaactctcnc ttctccacac gagcctttcg accatcactg 150  
 tccctgggtg gggaattgtg ttggaaagag gaactaccgc tantttctac 200  
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 atcgt 255

<310> 517  
 <311> 24  
 <312> DNA  
 <313> Artificial Sequence

<320>  
 <321> Synthetic oligonucleotide probe

<400> 517  
 caacgtgatt tcaaagctgg gctc 24

<310> 518  
 <311> 29  
 <312> DNA  
 <313> Artificial Sequence

<320>  
 <321> Synthetic oligonucleotide probe

<400> 518

gactcgtatc aagaatttc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtgagaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctctactgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

ccgcacaaaccc attttgggag caggaattcc aatcatgtct gtgatggtyg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaa ccattccagc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

ctgtgtctctt ccaaggagtg ccgtggcgca gaggagatgc caacttcccc 250

caagctatgg acaacgtgac ggtccggcag ggggagagcg ccacccctcag 300

gtgcactatt gacaacgggg ccacccgggt ggctggcta aacgcagca 350

ccatctctta tctgtgggaat gacaagtggg gctggatcc tcgctggtgc 400



tttctgagca acaccccaaac gcagtagagc atcgagatcc agaacgtgga 450  
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 gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600  
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 acactgcagt gtgaagcctc agcagtcacc tcagcagaat tcagtggtta 900  
 caaggatgac aaaagactga ttgaaggaaa gaaagggtg aaagtggaaa 950  
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(210) • 523  
 (211) • 344  
 (212) • PRT  
 (213) • Homo sapiens

<400> 523

Met	Lys	Thr	Ile	Gln	Pro	Lys	Met	His	Asn	Ser	Ile	Ser	Trp	Ala	1	5	10	15
Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro	20	25	30	35
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	40	45	50	55
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	60	65	70	75
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	80	85	90	95
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	100	105	110	115
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	120	125	130	135
Asp	Val	Tyr	Asp	Gln	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	140	145	150	155
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	160	165	170	175
Pro	Lys	Ile	Val	Gln	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	180	185	190	195
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	200	205	210	215
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	220	225	230	235
Ser	Glu	Asp	Gln	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	240	245	250	255
Ser	Gly	Asp	Tyr	Gln	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	260	265	270	275
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	280	285	290	295
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	300	305	310	315
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	320	325	330	335
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	340	345	350	355
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	360	365	370	375

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys  
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Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala  
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val  
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe  
335 340

CL10: 514  
CL11: 503  
CL12: DNA  
CL13: Homo sapiens

CL400: 514  
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 TGTTCGCAAC GGAGATGCCA CTTCCCCCAA AGCTATGGAC AACGTGACGG 150  
 TCCGTCAGGG GGAGAGGGCC ACGCTCAGGT GCATATTGA CAACGGGGTC 200  
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 TAG 503

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CL11: 2602  
CL12: DNA  
CL13: Homo sapiens

CL400: 505  
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<210> 526  
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<400> 526  
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 35 40 45  
 Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro  
 50 55 60

Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly	65	70	75
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Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	95	100	105
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Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	125	130	135
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Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro	155	160	165
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Glu	Pro	Val	Val	Val	Tyr	Gly	Met	Asp	Tyr	Leu	Gln	Gln	Val	Ser	335	340	345

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Lys	Lys	Ser	Cys	Val	Pro	Arg	Trp	Gln	Thr	Cys	Ile	Ser	Asn	Thr	395	400	405
Asp	Asp	Ala	Leu	Gly	Phe	Ala	Leu	Gly	Ser	Leu	Phe	Val	Lys	Ala	410	415	420
Thr	Phe	Asp	Arg	Gln	Ser	Lys	Glu	Ile	Ala	Glu	Gly	Met	Ile	Ser	425	430	435
Glu	Ile	Arg	Thr	Ala	Phe	Gln	Glu	Ala	Leu	Gly	Gln	Leu	Val	Trp	440	445	450
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Tyr	Asp	Lys	Glu	Gly	Asn	Leu	Arg	Pro	Trp	Trp	Gln	Asn	Glu	Ser	590	595	600
Leu	Ala	Ala	Phe	Arg	Asn	His	Thr	Ala	Tys	Met	Glu	Glu	Gln	Tyr	605	610	615
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Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His
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Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val
				695					700					705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly
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Cys	Pro	Val	Gly	Ser	Pro	Met	Asn	Pro	Gly	Gln	Leu	Cys	Glu	Val
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Trp

+010 - 527  
 +011 - 4008  
 +012 - DNA  
 +013 - Homo sapiens

+020 -  
 +021 - unsure  
 +022 - 1473, 3373, 4057-4058, 4070  
 +023 - unknown base

+040 - 527  
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(220)

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4211. 26

4212. DNA

4213. Artificial Sequence

4222.

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4210. 596

4211. 31

4212. DNA

4213. Artificial Sequence

4223.

4223. Synthetic oligonucleotide probe

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 aaaaaagaat attgcagtcg atatgtgatt ctttaaggct gcaatacaag 1750  
 cattcagttc cctgttttcaa caagagtcba tcacattta caaagatgca 1800  
 tttttttctt ctttgataaa aaagcaata atattgcctc cagattattt 1850  
 cttcaaaaata taacacatat cttagatttt ctgcttgcat gatattcag 1900  
 tttcaggaat gacccctgta atataactgg ctgtgcagct ctgcttctct 1950  
 tctctgtaag ttcagcatgg gtgtgccttc atacaataat attttctctt 2000  
 ctgtctccaa ctaacataaa atgttttgtt aaatcttaca atttgaaagt 2050  
 aaaaataaac cagagtcgac aagttaaacc atacactatc tctaagtaac 2100  
 gaaggagcta ttggactgta aaaatctctt cctgcactga caatggggtt 2150

tgagaatttt gccccacact aactcagttc ttgtgatgag agacaattta 2200  
 ataacagtat agtaaatata ccatatgatt tottttagttg tagctaaatg 2250  
 ttagatccac cgtgggaaat cattcccttt aaaatgacag cacagtccac 2300  
 tcaaaggatt gcctagcaat acagcatctt ttcccttcac tagtccaagc 2350  
 caaaaatttt aagatgattt gtcagaaagg gcacaaagtc ctatcaocta 2400  
 atattacaag agtttgtaag cgtccatcat taattttatt ttgtggcag 2450  
 tattatgaca gtccagctgg aggggatgga tatggatatg gacgttcac 2500  
 agactataat ggcagaaacc aggggtggtta tgacccgtac tcaggaggaa 2550  
 attacagaga caattatgac aactgaaatg agacatgcac ataatataga 2600  
 tacacaagga ataattcttg atccaggatc gtccctccaa atggctgtat 2650  
 ttataaaggt ttttgagct gcactgaagc atcttatctt atagtatctc 2700  
 aaccttttgt ttttaaattg aacctgccaag gtagctgaag acctttttaga 2750  
 cagttccatc ctttttttta aattttttct gctattttaa agacaaatta 2800  
 tgggaagttt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612  
 <211> 352  
 <212> PRT  
 <213> Homo Sapien

<400> 612  
 Met Met Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln Trp Leu  
 1 5 10 15  
 Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser Cys Leu  
 20 25 30  
 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn  
 35 40 45  
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu  
 50 55 60  
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile  
 65 70 75  
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser  
 80 85 90  
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn  
 95 100 105  
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu		
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu		
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe		
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln		
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro		
200	205	210
Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile		
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu		
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu Trp		
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile		
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val		
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys		
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr		
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys		
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile Phe Tyr		
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613  
 <211> 1797  
 <212> DNA  
 <213> Homo Sapien

<400> 613  
 agtgggttoga tgggaaggat ctttctccaa gtggttcttc ttgaggggag 50



cattttctgct ggctccagga ctttggccat ctataaagct tggcaatgag 100  
aaataagaaa atttccaagg aggaacgagct cttgagttag acccaacaag 150  
ctggttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
cccaagagga gaaatggggg gaactttccc ctagctgtgg tggtcattcta 250  
cccgatcctg ctccacgctg gggctggggc gctgggtggc caagtcttga 300  
atctgcaggc ggggtccgg gtccctggaga tgtatttccct caatgacact 350  
ctgggggctg aggaacagcc gtcccttccc ttgctgcagt cagcacaccc 400  
tggagaacac ctgggtcagg gtgcctcgag gctgcaagtc ctgcaggccc 450  
aactcaactg ggtccgctc agccatgagc aattgctgca ggggttagac 500  
aacttcaact agaaccaggt gatgttcaga atcaaaaggtg aacaaggcgc 550  
ccaggtctt caaggtcaca agggggccat gggcatgctt ggtgcacctg 600  
gcccgcgggg accacctgct gagaaggag aggaaggggc tatgggacga 650  
gatggagcaa caggccacct gggaccccaa gggccacggg gagtcaaggg 700  
agaggcgggc cccaaggac ccaggggtgc tccagggag caaggagcca 750  
ctggcacccc aggaacccaa ggagagaagg gcagcaagg cgatgggggt 800  
ctcattggcc caaaaggga aactggaaat aagggagaga aaggagacct 850  
gggtctccca ggaagcaag gggacaggg catgaaagga gatgcagggg 900  
tcattggggc tcttgagcc caggggagta aaggtagact cgggagggca 950  
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gtgccaaggg ttagccctgg agtgcctggc cccctgggcy agcaggacct 1100  
ccagggagcc ccgggagtcc aggagccaca ggcctgaaag gaagcaagg 1150  
ggacacagga cttcaaggac agcaaggag aaaaggagaa ccaggagtcc 1200  
caggccctgc aggtgtgaa ggagaacagg gtagccbagy gctggcaggt 1250  
cccaagggag cccctggaca agctggccag aagggagacc agggagtcaa 1300  
aggatcttct ggggagcaag gagtcaagg agaaaaaggt gaaagaggtg 1350  
aaaactcagt gtcctcagg attgtcggca gtagtaacct aggcggggct 1400  
gaagtctact acagtggtao ctgggggaca atttgcgatg acgagtggca 1450

aaattctgat gccatttgtt ttgtccgcat gctgggttac tccaaaggaa 1500  
 gggccctgtt caaagtggga gctggcactg ggcagatctg gctggataat 1550  
 gtcagtgctt ggggcacgga gactaccttg tggagctgca ccaagaatag 1600  
 ctgggggcat catgactgca gccacgagga ggacgcagga gtggagtcca 1650  
 ggtctgacc cggaaacctt ttcactctc tgcctccag gtgtccctgg 1700  
 gctcatatgt gggaaggcag aggatctctg aggagttccc tggggacaa 1750  
 tcagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614  
 <211> 520  
 <212> PRT  
 <213> Homo Sapien

<410> 614  
 Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu  
 1 5 10 15  
 Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu  
 20 25 30  
 Ile Asn Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser  
 35 40 45  
 Leu Ala Val Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala  
 50 55 60  
 Gly Leu Leu Val Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg  
 65 70 75  
 Val Leu Glu Met Tyr Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp  
 80 85 90  
 Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His Pro Gly Glu His  
 95 100 105  
 Leu Ala Gln Gly Ala Ser Arg Leu Gln Val Leu Gln Ala Gln Leu  
 110 115 120  
 Thr Trp Val Arg Val Ser His Glu His Leu Leu Gln Arg Val Asp  
 125 130 135  
 Asn Phe Thr Gln Asn Pro Gly Met Phe Arg Ile Lys Gly Glu Gln  
 140 145 150  
 Gly Ala Pro Gly Leu Gln Gly His Lys Gly Ala Met Gly Met Pro  
 155 160 165  
 Gly Ala Pro Gly Pro Pro Gly Pro Pro Ala Glu Lys Gly Ala Lys  
 170 175 180  
 Gly Ala Met Gly Arg Asp Gly Ala Thr Gly Pro Ser Gly Pro Gln

125	130	135
Gly Pro Pro Gly Val Lys Gly Glu Ala	Gly Leu Gln Gly Pro Gln	
200	205	210
Gly Ala Pro Gly Lys Gln Gly Ala Thr	Gly Thr Pro Gly Pro Gln	
215	220	225
Gly Glu Lys Gly Ser Lys Gly Asp Gly	Gly Leu Ile Gly Pro Lys	
230	235	240
Gly Glu Thr Gly Thr Lys Gly Glu Lys	Gly Asp Leu Gly Leu Pro	
245	250	255
Gly Ser Lys Gly Asp Arg Gly Met Lys	Gly Asp Ala Gly Val Met	
260	265	270
Gly Pro Pro Gly Ala Gln Gly Ser Lys	Gly Asp Phe Gly Arg Pro	
275	280	285
Gly Pro Pro Gly Leu Ala Gly Phe Pro	Gly Ala Lys Gly Asp Gln	
290	295	300
Gly Gln Pro Gly Leu Gln Gly Val Pro	Gly Pro Pro Gly Ala Val	
305	310	315
Gly His Pro Gly Ala Lys Gly Glu Pro	Gly Ser Ala Gly Ser Pro	
320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	

470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu		
485	490	495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His		
500	505	510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val		
515	520	

<210> 615  
 <211> 647  
 <212> DNA  
 <213> Homo Sapien

<400> 615  
 cccacgggtc cgaaggcaga caaaggttca ttgttaaaga agtccttcc 50  
 agcaactcct ctcttctcct ttgtcccaaa ctccaccagt gagtgtgagc 100  
 atttaagaag catctctctgc caagaccaaa aggaaagaag aaaaaggggc 150  
 aaaagccaaa atgaaaactga tggtaacttgt ttccaccatt gggctaactt 200  
 tgcctgtagg agttcaagcc atgcttgcaa atgctctctc ttgtacaga 250  
 aagatactaa aagatccaaa ctgtcccaac ctcccggaag gagttagctga 300  
 cctgacacag attgagtcca atgtccagga tcattctctgg gatgggaagg 350  
 gatgtgagat gatctgttac tgcaacttca gogaattgct ctgtcgccca 400  
 aaagacgttt tctttggacc aaagatctct ttctgtgattc ctgtcaacaa 450  
 tcaatgagaa tcttcattga ttctggagaa caccattcct gatttcacac 500  
 aaactgcact acatcagtat aactgcattt ctagtcttcta tatagtgcac 550  
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaatctgt 600  
 gttcaacaaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616  
 <211> 34  
 <212> PRT  
 <213> Homo Sapien

<400> 616
Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
1 5 10 15
Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
20 25 30
Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50				55						60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65				70						75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80				85						90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<110> 617  
 <111> 2558  
 <112> DNA  
 <113> Homo Sapien

<400> 617  
 cccacgggtc cgggacggg tgggtggac cccaggtctg gagcgaattc 50  
 cagcctgcag ggtgataag cgaggcatta gtgagattga gagagacttc 100  
 acccggcgtt ggtgggttga gggcgcgag tagagcagca gcacaggcgc 150  
 gggtcgggg aggcgggtc cgtcgcgcc gagatgtga atctcttca 200  
 cgaaacgac tgggtgtgg ccacggcgcg cggcggcgc tgggtgtgag 250  
 ctggggcgct ggtgtggcg ggtggcttct ctctctcgg ctctctcttc 300  
 ggggtggtta taaaatcttc caatgaagct actaacatta ctccaaaaga 350  
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400  
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaaa 450  
 tttcagcttg caaagcaaat tcaatccag tggaaagaat ttggcctgga 500  
 ctctgttgag ctagctcatt atgatgtctt gctgtctctc ccaataaga 550  
 ctcatcccaa ctacatctca ataattaatg aagatggaaa cgagattctc 600  
 aacacatcat tatttgaac accctctcca ggatatgaaa atgtctcgga 650  
 tattgtacca ccttcagtg cttctctctc tcaagggaatg ccagagggcg 700  
 atctagtgtg tgttaactat gcaagaaatg aagaattctt taaattggaa 750  
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800  
 gaaagtcttc agaggaaata aggttaaaaa cgcacagctg gcaggggcga 850  
 aaggagtcac ctctactctc gacctgctg actactttgc tctgggggtg 900  
 aagtcctatc cagacgggtg gaatcttctt ggaggtggtg tccagcttgg 950

aaatatccta aatctgaatg gtgcaggaga cccctctaca ccagggttacc 1000  
cagcaaatga atatgcttat agggctggaa ttgcagagge tgttggctct 1050  
ccaagtatc ctgttcctcc aattggatac tatgatgcac agaagctcct 1100  
agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150  
ccaaagtgc ctacaatgtt ggacctggct ttactggaaa cttctctaca 1200  
caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250  
caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300  
ttctgggagg ccacggggac ccctgggtgt ttggtggctat tgacctcag 1350  
agtggagcag ctgttgtctc tgaaattgtg aggagctttg gaacctgaa 1400  
aaaggaaggg tggagaccta gaagaacaat tttgtttgca agctgggatg 1450  
cagaagaatt tggctctctt ggttctactg agtgggcaga ggagaattca 1500  
agaactcttc aagagctgg cgtggcttat attaatgctg actcatctat 1550  
agaaggaaac taccctctga gagctgattg taccctctg atgtacagct 1600  
tggtaacaca cctaacaaaa gagctgaaaa gacctgatga aggtcttgaa 1650  
ggcaaatctt tttatgaaag ttggactaaa aaaagtctct cccagagtt 1700  
cagtggcatg cccaggataa gcaaatggg acctggaaat gattctgagg 1750  
tgtctctcca accacttgga attgcttcag gcagagcacg gtatactaaa 1800  
aattgggaaa caaaccaatt cagcggctat ccactgtatc acagtgtcta 1850  
tgaaacatat gagtgggtgg aaaagtctta tgatccaatg cttaaatctc 1900  
acctcactgt ggcccaggtt cgaggagggg tgggtttga gctagccaat 1950  
tcctagtgc ccccttttga ttgtcgagat tatgctgtat ctttaagaaa 2000  
gtatgtgac aaaatctaca gtattctctat gaaacatcca caggaaatga 2050  
agacatacag tgtatcattt gattcacttt tctctgcagt aaagaatttt 2100  
acagaaattg ctcccaagtt cagtgcagaga cccaggact ttgacaaaag 2150  
caacccaata gtattaagaa tgatgaatga ccaactcctg tttctggaaa 2200  
gagcatttat tgatccaata gggttaccag acaggccttt ctataggcat 2250  
gcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300  
aggaatttat gatgctctgt ttgatattga aagcaaatg gacctctca 2350  
aggctgggg agaagtgaag agacagattt atgttgacgc ctccacagtg 2400

caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450  
 gaatccgtat tgaatttggtg tggatatgtca ctacagaaaga atcgtaatgg 2500  
 gtatatattgat aaatttttaaa attggtatat ttgaaataaa gttgaatatt 2550  
 atatataa 2553

<210> 618  
 <211> 750  
 <212> PRT  
 <213> Homo Sapien

<400> 618  
 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala  
 1 5 10 15  
 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly  
 20 25 30  
 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser  
 35 40 45  
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala  
 50 55 60  
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His  
 65 70 75  
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe  
 80 85 90  
 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu  
 95 100 105  
 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro  
 110 115 120  
 Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly  
 125 130 135  
 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly  
 140 145 150  
 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser  
 155 160 165  
 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala  
 170 175 180  
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn  
 185 190 195  
 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg  
 200 205 210

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu	485	490	495



Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	500	505	510
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	515	520	525
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	530	535	540
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	545	550	555
Tyr	Glu	Thr	Tyr	Gln	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	560	565	570
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	575	580	585
Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	590	595	600
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser	605	610	615
Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp	620	625	630
Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys	635	640	645
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val	650	655	660
Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	Arg	Ala	Phe	665	670	675
Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val	680	685	690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe	695	700	705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp	710	715	720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala	725	730	735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala	740	745	750

<213> 19

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

4223 Synthetic oligonucleotide probe

4400 619

agatgttaag gtgcaggtgt gccg 24

4210 610

4211 18

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 620

gaatatcagc gctccggta attcc 25

4210 621

4211 46

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 621

ccagctttg aatggtaccg aggagagaag aagctcttca atggcc 46

4210 622

4211 26

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 622

ccaaatcac ccagtgagtg tgagc 25

4210 623

4211 25

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic oligonucleotide probe

4400 623

ggggaatca ggaatggtgt tctcc 25

4210 624

4211 40

4212 DNA

4213 Artificial Sequence

4220

4223 Synthetic Oligonucleotide probe

<400> 624

cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50